

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Ish-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
Gray, Grace

(ii) TITLE OF THE INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
AND FRAGMENTS

(iii) NUMBER OF SEQUENCES: 94

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Pennie & Edmonds LLP
(B) STREET: 1155 Avenue of the Americas
(C) CITY: New York
(D) STATE: NY
(E) COUNTRY: USA
(F) ZIP: 10036/2711

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: TO BE ASSIGNED
(B) FILING DATE: ON AN EVEN DATE HEREWITH
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/981,392
(B) FILING DATE: 22-DEC-1997
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Antler, Adriane M.
(B) REGISTRATION NUMBER: 32,605
(C) REFERENCE/DOCKET NUMBER: 7326-122

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 212-790-9090
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2508 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 277...2460

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGCA CGAGGTTTTT TTTTTTTTTT TTCCCCTCTT TTCTTTCTTT TCCTTTTGCC 60
ATCCGAAAGA GCTGTCAGCC GCCGCCGGGC TGCACCTAAA GCGTCGGTA GGGGGATAAC 120
AGTCAGAGAC CCTCCTGAAA GCAGGAGACG GGACGGTACC CCTCCGGCTC TCGGGGCGG 180
CTGCGGCCCC TCCGTTCTTT CCCCCTCCCC GAGAGACACT CTTCTTTCC CCCCACGAAG 240
ACACAGGGGC AGGAACGCGA GCGCTGCCCC TCCGCC ATG GGA GGC CGC TTC CTG 294
Met Gly Gly Arg Phe Leu
1 5

CTG ACG CTC GCC CTC CTC TCG GCG CTG CTG TGC CGC TGC CAG GTT GAC 342
Leu Thr Leu Ala Leu Leu Ser Ala Leu Leu Cys Arg Cys Gln Val Asp
10 15 20

GGC TCC GGG GTG TTC GAG CTG AAG CTG CAG GAG TTT GTC AAC AAG AAG 390
Gly Ser Gly Val Phe Glu Leu Lys Leu Gln Glu Phe Val Asn Lys Lys
25 30 35

GGG CTG CTC AGC AAC CGC AAC TGC TGC CGG GGG GGC GGC CCC GGA GGC 438
Gly Leu Leu Ser Asn Arg Asn Cys Cys Arg Gly Gly Gly Pro Gly Gly
40 45 50

GCC GGG CAG CAG CAG TGC GAC TGC AAG ACC TTC TTC CGC GTC TGC CTG 486
Ala Gly Gln Gln Gln Cys Asp Cys Lys Thr Phe Phe Arg Val Cys Leu
55 60 65 70

AAG CAC TAC CAG GCC AGC GTC TCC CCC GAG CCG CCC TGC ACC TAC GGC 534
Lys His Tyr Gln Ala Ser Val Ser Pro Glu Pro Pro Cys Thr Tyr Gly
75 80 85

AGC GCC ATC ACC CCC GTC CTC GGC GCC AAC TCC TTC AGC GTC CCC GAC 582
Ser Ala Ile Thr Pro Val Leu Gly Ala Asn Ser Phe Ser Val Pro Asp
90 95 100

GGC GCG GGC GGC GCC GAC CCC GCC TTC AGC AAC CCC ATC CGC TTC CCC 630
Gly Ala Gly Gly Ala Asp Pro Ala Phe Ser Asn Pro Ile Arg Phe Pro
105 110 115

TTC GGC TTC ACC TGG CCC GGC ACC TTC TCG CTC ATC ATC GAG GCT CTG 678
Phe Gly Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Ala Leu
120 125 130

CAC ACC GAC TCC CCC GAC GAC CTC ACC ACA GAA AAC CCC GAG CGC CTC 726
His Thr Asp Ser Pro Asp Asp Leu Thr Thr Glu Asn Pro Glu Arg Leu
135 140 145 150

ATC AGC CGC CTG GCC ACC CAG AGG CAC CTG GCG GTG GGC GAG GAG TGG 774
Ile Ser Arg Leu Ala Thr Gln Arg His Leu Ala Val Gly Glu Glu Trp

155

160

165

TCC CAG GAC CTG CAC AGC AGC GGC CGC ACC GAC CTC AAG TAC TCC TAT	822
Ser Gln Asp Leu His Ser Ser Gly Arg Thr Asp Leu Lys Tyr Ser Tyr	
170 175 180	
CGC TTT GTG TGT GAT GAG CAC TAC TAC GGG GAA GGC TGC TCT GTC TTC	870
Arg Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe	
185 190 195	
TGC CGG CCC CGT GAC GAC CGC TTC GGT CAC TTC ACC TGT GGA GAG CGT	918
Cys Arg Pro Arg Asp Asp Arg Phe Gly His Phe Thr Cys Gly Glu Arg	
200 205 210	
GGC GAG AAG GTC TGC AAC CCA GGC TGG AAG GGC CAG TAC TGC ACT GAG	966
Gly Glu Lys Val Cys Asn Pro Gly Trp Lys Gly Gln Tyr Cys Thr Glu	
215 220 225 230	
CCG ATT TGC TTG CCT GGG TGT GAC GAG CAG CAC GGC TTC TGC GAC AAA	1014
Pro Ile Cys Leu Pro Gly Cys Asp Glu Gln His Gly Phe Cys Asp Lys	
235 240 245	
CCT GGG GAA TGC AAG TGC AGA GTG GGT TGG CAG GGG CGG TAC TGT GAC	1062
Pro Gly Glu Cys Lys Cys Arg Val Gly Trp Gln Gly Arg Tyr Cys Asp	
250 255 260	
GAG TGC ATC CGA TAC CCA GGC TGC CTG CAC GGT ACC TGT CAG CAG CCA	1110
Glu Cys Ile Arg Tyr Pro Gly Cys Leu His Gly Thr Cys Gln Gln Pro	
265 270 275	
TGG CAG TGC AAC TGC CAG GAA GGC TGG GGC GGC CTT TTC TGC AAC CAG	1158
Trp Gln Cys Asn Cys Gln Glu Gly Trp Gly Gly Leu Phe Cys Asn Gln	
280 285 290	
GAC CTG AAC TAC TGC ACT CAC CAC AAG CCA TGC AAG AAT GGT GCC ACA	1206
Asp Leu Asn Tyr Cys Thr His His Lys Pro Cys Lys Asn Gly Ala Thr	
295 300 305 310	
TGC ACC AAC ACC GGT CAG GGG AGC TAC ACT TGT TCT TGC CGA CCT GGG	1254
Cys Thr Asn Thr Gly Gln Gly Ser Tyr Thr Cys Ser Cys Arg Pro Gly	
315 320 325	
TAC ACA GGC TCC AGC TGC GAG ATT GAA ATC AAC GAA TGT GAT GCC AAC	1302
Tyr Thr Gly Ser Ser Cys Glu Ile Glu Ile Asn Glu Cys Asp Ala Asn	
330 335 340	
CCT TGC AAG AAT GGT GGA AGC TGC ACG GAT CTC GAG AAC AGC TAT TCC	1350
Pro Cys Lys Asn Gly Gly Ser Cys Thr Asp Leu Glu Asn Ser Tyr Ser	
345 350 355	
TGT ACC TGC CCC CCA GGC TTC TAT GGT AAA AAC TGT GAG CTG AGT GCA	1398
Cys Thr Cys Pro Pro Gly Phe Tyr Gly Lys Asn Cys Glu Leu Ser Ala	
360 365 370	
ATG ACT TGT GCT GAT GGA CCG TGC TTC AAT GGA GGG CGA TGC ACT GAC	1446
Met Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Arg Cys Thr Asp	
375 380 385 390	

AAC CCT GAT GGT GGA TAC AGC TGC CGC TGC CCA CTG GGT TAT TCT GGG	1494
Asn Pro Asp Gly Gly Tyr Ser Cys Arg Cys Pro Leu Gly Tyr Ser Gly	
395 400 405	
TTC AAC TGT GAA AAG AAA ATC GAT TAC TGC AGT TCC AGC CCT TGT GCT	1542
Phe Asn Cys Glu Lys Lys Ile Asp Tyr Cys Ser Ser Ser Pro Cys Ala	
410 415 420	
AAT GGA GCC CAG TGC GTT GAC CTG GGG AAC TCC TAC ATA TGC CAG TGC	1590
Asn Gly Ala Gln Cys Val Asp Leu Gly Asn Ser Tyr Ile Cys Gln Cys	
425 430 435	
CAG GCT GGC TTC ACT GGC AGG CAC TGT GAC GAC AAC GTG GAC GAT TGC	1638
Gln Ala Gly Phe Thr Gly Arg His Cys Asp Asp Asn Val Asp Asp Cys	
440 445 450	
GCC TCC TTC CCC TGC GTC AAT GGA GGG ACC TGT CAG GAT GGG GTC AAC	1686
Ala Ser Phe Pro Cys Val Asn Gly Gly Thr Cys Gln Asp Gly Val Asn	
455 460 465 470	
GAC TAC TCC TGC ACC TGC CCC CCG GGA TAC AAC GGG AAG AAC TGC AGC	1734
Asp Tyr Ser Cys Thr Cys Pro Pro Gly Tyr Asn Gly Lys Asn Cys Ser	
475 480 485	
ACG CCG GTG AGC AGA TGC GAG CAC AAC CCC TGC CAC AAT GGG GCC ACC	1782
Thr Pro Val Ser Arg Cys Glu His Asn Pro Cys His Asn Gly Ala Thr	
490 495 500	
TGC CAC GAG AGA AGC AAC CGC TAC GTG TGC GAG TGC GCT CGG GGC TAC	1830
Cys His Glu Arg Ser Asn Arg Tyr Val Cys Glu Cys Ala Arg Gly Tyr	
505 510 515	
GGC GGC CTC AAC TGC CAG TTC CTG CTC CCC GAG CCA CCT CAG GGG CCG	1878
Gly Gly Leu Asn Cys Gln Phe Leu Leu Pro Glu Pro Pro Gln Gly Pro	
520 525 530	
GTC ATC GTT GAC TTC ACC GAG AAG TAC ACA GAG GGC CAG AAC AGC CAG	1926
Val Ile Val Asp Phe Thr Glu Lys Tyr Thr Glu Gly Gln Asn Ser Gln	
535 540 545 550	
TTT CCC TGG ATC GCA GTG TGC GCC GGG ATT ATT CTG GTC CTC ATG CTG	1974
Phe Pro Trp Ile Ala Val Cys Ala Gly Ile Ile Leu Val Leu Met Leu	
555 560 565	
CTG CTG GGT TGC GCC GCC ATC GTC GTC TGC GTC AGG CTG AAG GTG CAG	2022
Leu Leu Gly Cys Ala Ala Ile Val Val Cys Val Arg Leu Lys Val Gln	
570 575 580	
AAG AGG CAC CAC CAG CCC GAG GCC TGC AGG AGT GAA ACG GAG ACC ATG	2070
Lys Arg His His Gln Pro Glu Ala Cys Arg Ser Glu Thr Glu Thr Met	
585 590 595	
AAC AAC CTG GCG AAC TGC CAG CGC GAG AAG GAC ATC TCC ATC AGC GTC	2118
Asn Asn Leu Ala Asn Cys Gln Arg Glu Lys Asp Ile Ser Ile Ser Val	
600 605 610	
ATC GGT GCC ACT CAG ATT AAA AAC ACA AAT AAG AAA GTA GAC TTT CAC	2166
Ile Gly Ala Thr Gln Ile Lys Asn Thr Asn Lys Lys Val Asp Phe His	

615	620	625	630	
AGC GAT AAC TCC GAT AAA AAC GGC TAC AAA GTT AGA TAC CCA TCA GTG				2214
Ser Asp Asn Ser Asp Lys Asn Gly Tyr Lys Val Arg Tyr Pro Ser Val	635	640	645	
GAT TAC AAT TTG GTG CAT GAA CTC AAG AAT GAG GAC TCT GTG AAA GAG				2262
Asp Tyr Asn Leu Val His Glu Leu Lys Asn Glu Asp Ser Val Lys Glu	650	655	660	
GAG CAT GGC AAA TGC GAA GCC AAG TGT GAA ACG TAT GAT TCA GAG GCA				2310
Glu His Gly Lys Cys Glu Ala Lys Cys Glu Thr Tyr Asp Ser Glu Ala	665	670	675	
GAA GAG AAA AGC GCA GTA CAG CTA AAA AGT AGT GAC ACT TCT GAA AGA				2358
Glu Glu Lys Ser Ala Val Gln Leu Lys Ser Ser Asp Thr Ser Glu Arg	680	685	690	
AAA CGG CCA GAT TCA GTA TAT TCC ACT TCA AAG GAC ACA AAG TAC CAG				2406
Lys Arg Pro Asp Ser Val Tyr Ser Thr Ser Lys Asp Thr Lys Tyr Gln	695	700	705	710
TCG GTG TAC GTC ATA TCA GAA GAG AAA GAT GAG TGC ATC ATA GCA ACT				2454
Ser Val Tyr Val Ile Ser Glu Glu Lys Asp Glu Cys Ile Ile Ala Thr	715	720	725	
GAG GTG TAAACAGAC GTGACGTGGC AAAGCTTATC GATACCGTCA TCAAGCTT				2508
Glu Val				

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 728 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gly	Gly	Arg	Phe	Leu	Leu	Thr	Leu	Ala	Leu	Leu	Ser	Ala	Leu	Leu
1				5					10					15	
Cys	Arg	Cys	Gln	Val	Asp	Gly	Ser	Gly	Val	Phe	Glu	Leu	Lys	Leu	Gln
			20					25					30		
Glu	Phe	Val	Asn	Lys	Lys	Gly	Leu	Leu	Ser	Asn	Arg	Asn	Cys	Cys	Arg
			35				40					45			
Gly	Gly	Gly	Pro	Gly	Gly	Ala	Gly	Gln	Gln	Gln	Cys	Asp	Cys	Lys	Thr
			50			55					60				
Phe	Phe	Arg	Val	Cys	Leu	Lys	His	Tyr	Gln	Ala	Ser	Val	Ser	Pro	Glu
65					70				75					80	
Pro	Pro	Cys	Thr	Tyr	Gly	Ser	Ala	Ile	Thr	Pro	Val	Leu	Gly	Ala	Asn
				85					90				95		
Ser	Phe	Ser	Val	Pro	Asp	Gly	Ala	Gly	Gly	Ala	Asp	Pro	Ala	Phe	Ser
			100				105						110		
Asn	Pro	Ile	Arg	Phe	Pro	Phe	Gly	Phe	Thr	Trp	Pro	Gly	Thr	Phe	Ser

Val	Arg	Leu	Lys	Val	Gln	Lys	Arg	His	His	Gln	Pro	Glu	Ala	Cys	Arg
			580					585					590		
Ser	Glu	Thr	Glu	Thr	Met	Asn	Asn	Leu	Ala	Asn	Cys	Gln	Arg	Glu	Lys
		595					600					605			
Asp	Ile	Ser	Ile	Ser	Val	Ile	Gly	Ala	Thr	Gln	Ile	Lys	Asn	Thr	Asn
	610					615					620				
Lys	Lys	Val	Asp	Phe	His	Ser	Asp	Asn	Ser	Asp	Lys	Asn	Gly	Tyr	Lys
625					630					635					640
Val	Arg	Tyr	Pro	Ser	Val	Asp	Tyr	Asn	Leu	Val	His	Glu	Leu	Lys	Asn
				645					650					655	
Glu	Asp	Ser	Val	Lys	Glu	Glu	His	Gly	Lys	Cys	Glu	Ala	Lys	Cys	Glu
			660					665					670		
Thr	Tyr	Asp	Ser	Glu	Ala	Glu	Glu	Lys	Ser	Ala	Val	Gln	Leu	Lys	Ser
		675					680					685			
Ser	Asp	Thr	Ser	Glu	Arg	Lys	Arg	Pro	Asp	Ser	Val	Tyr	Ser	Thr	Ser
	690					695					700				
Lys	Asp	Thr	Lys	Tyr	Gln	Ser	Val	Tyr	Val	Ile	Ser	Glu	Glu	Lys	Asp
705					710					715					720
Glu	Cys	Ile	Ile	Ala	Thr	Glu	Val								
															725

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCGGCA	CGAGGTTTTT	TTTTTTTTTT	TTCCCCTCTT	TTCTTTCTTT	TCCTTTTGCC	60
ATCCGAAAGA	GCTGTCAGCC	GCCGCCGGGC	TGCACCTAAA	GGCGTCGGTA	GGGGGATAAC	120
AGTCAGAGAC	CCTCCTGAAA	GCAGGAGACG	GGACGGTACC	CCTCCGGCTC	TGCGGGGCGG	180
CTGCGGCCCC	TCCGTTCTTT	CCCCCTCCCC	GAGAGACACT	CTTCCTTTCC	CCCCACGAAG	240
ACACAGGGGC	AGGAACGCGA	GCGCTGCCCC	TCCGCCATGG	GAGGCGGCTT	CCTGCTGACG	300
CTCGCCCTCC	TCTCGGCGCT	GCTGTGCCGC	TGCCAGGTTG	ACGGCTCCGG	GGTGTTGAG	360
CTGAAGCTGC	AGGAGTTTGT	CAACAAGAAG	GGGCTGCTCA	GCAACCGCAA	CTGCTGCCGG	420
GGGGGCGGCC	CCGGAGGCGC	CGGGCAGCAG	CAGTGCGACT	GCAAGACCTT	CTTCCGCGTC	480
TGCCTGAAGC	ACTACCAGGC	CAGCGTCTCC	CCCGAGCCGC	CCTGCACCTA	CGGCAGCGCC	540
ATCACCCCG	TCCTCGGCGC	CAACTCCTTC	AGCGTCCCCG	ACGGCGCGGG	CGGCGCCGAC	600
CCCGCCTTCA	GCAACCCCAT	CCGCTTCCCC	TTCGGCTTCA	CCTGGCCCGG	CACCTTCTCG	660
CTCATCATCG	AGGCTCTGCA	CACCGACTCC	CCCGACGACC	TCACCACAGA	AAACCCCGAG	720
CGCCTCATCA	GCCGCCTGGC	CACCCAGAGG	CACCTGGCGG	TGGGCGAGGA	GTGGTCCCAG	780
GACCTGCACA	GCAGCGGCCG	CACCGACCTC	AAGTACTCCT	ATCGCTTTGT	GTGTGATGAG	840
CACTACTACG	GGGAAGGCTG	CTCTGTCTTC	TGCCGGCCCC	GTGACGACCG	CTTCGGTCAC	900
TTCACCTGTG	GAGAGCGTGG	CGAGAAGGTC	TGCAACCCAG	GCTGGAAGGG	CCAGTACTGC	960
ACTGAGCCGA	TTTGCTTGCC	TGGGTGTGAC	GAGCAGCACG	GCTTCTGCGA	CAAACCTGGG	1020
GAATGCAAGT	GCAGAGTGGG	TTGGCAGGGG	CGGTACTGTG	ACGAGTGCAT	CCGATACCCA	1080
GGCTGCCTGC	ACGGTACCTG	TCAGCAGCCA	TGGCAGTGCA	ACTGCCAGGA	AGGCTGGGGC	1140
GGCCTTTTCT	GCAACCAGGA	CCTGAACTAC	TGCACTCACC	ACAAGCCATG	CAAGAATGGT	1200
GCCACATGCA	CCAACACCGG	TCAGGGGAGC	TACACTTGTT	CTTGCCGACC	TGGGTACACA	1260
GGCTCCAGCT	GCGAGATTGA	AATCAACGAA	TGTGATGCCA	ACCCTTGCAA	GAATGGTGGA	1320
AGCTGCACGG	ATCTCGAGAA	CAGCTATTCC	TGTACCTGCC	CCCCAGGCTT	CTATGGTAAA	1380
AACTGTGAGC	TGAGTGCAAT	GACTTGTGCT	GATGGACCGT	GCTTCAATGG	AGGGCGATGC	1440
ACTGACAACC	CTGATGGTGG	ATACAGCTGC	CGCTGCCCAC	TGGGTATTTC	TGGGTTC AAC	1500

TGTGAAAAGA	AAATCGATTA	CTGCAGTTCC	AGCCCTTGTG	CTAATGGAGC	CCAGTGC GTT	1560
GACCTGGGGA	ACTCCTACAT	ATGCCAGTGC	CAGGCTGGCT	TCACTGGCAG	GCACTGTGAC	1620
GACAACGTGG	ACGATTGCGC	CTCCTTCCCC	TGCGTCAATG	GAGGGACCTG	TCAGGATGGG	1680
GTCAACGACT	ACTCCTGCAC	CTGCCCCCGG	GGATACAACG	GGAAGAACTG	CAGCACGCCG	1740
GTGAGCAGAT	GCGAGCACAA	CCCCTGCCAC	AATGGGGCCA	CCTGCCACGA	GAGAAGCAAC	1800
CGCTACGTGT	GCGAGTGC GC	TCGGGGCTAC	GGCGGCCTCA	ACTGCCAGTT	CCTGCTCCCC	1860
GAGCCACCTC	AGGGGCCGGT	CATCGTTGAC	TTCACCGAGA	AGTACACAGA	GGGCCAGAAC	1920
AGCCAGTTTC	CCTGGATCGC	AGTGTGCGCC	GGGATTATTC	TGGTCCTCAT	GCTGCTGCTG	1980
GGTTGCGCCG	CCATCGTCGT	CTGCGTCAGG	CTGAAGGTGC	AGAAGAGGCA	CCACCAGCCC	2040
GAGGCCTGCA	GGAGTGAAAC	GGAGACCATG	AACAACCTGG	CGAACTGCCA	GCGCGAGAAG	2100
GACATCTCCA	TCAGCGTCAT	CGGTGCCACT	CAGATTAAAA	ACACAAATAA	GAAAGTAGAC	2160
TTTCACAGCG	ATAACTCCGA	TAAAAACGGC	TACAAAGTTA	GATACCCATC	AGTGGATTAC	2220
AATTTGGTGC	ATGAACTCAA	GAATGAGGAC	TCTGTGAAAG	AGGAGCATGG	CAAATGCGAA	2280
GCCAAGTGTG	AAACGTATGA	TTCAGAGGCA	GAAGAGAAAA	GCGCAGTACA	GCTAAAAAGT	2340
AGTGACACTT	CTGAAAGAAA	ACGGCCAGAT	TCAGTATATT	CCACTTCAAA	GGACACAAAG	2400
TACCACTCGG	TGTACGTCAT	ATCAGAAGAG	AAAGATGAGT	GCATCATAGC	AACTGAGGTT	2460
AGTATCCCAC	CTGGCAGTCG	GACAAGTCTT	GGTGTGTGAT	TCCCATCCAG	CGCAGGTCAG	2520
GGCGGCCAAA	CCATTCTACC	TGCTGCCACA	GTCATCTGTA	CCCAATGAAA	ACTGGCCACC	2580
TTCAGTCTGT	GGCACTGCAG	ACGTTGAAAA	AACTTGTTGT	GGATTAACAT	AAGCTCCAGT	2640
GGGGGTTACA	GGGACAGCAA	TTTTTGCAGG	CAAGGGTATA	ACTGTAGTGC	AGTTGTAGCT	2700
TACTAACCCT	ACTGACTCAT	TCTTTCGTGT	GCTTCCTGCA	GAGCCTGTTT	TTGCTTGGCA	2760
TTGAGGTGAA	GTCCTGACCC	TCTGCATCCT	CATAGTCCTC	TGCTTTCCTT	TTATTAACCT	2820
CTTCTGGTCT	CTGCTTGTCT	TTTCTCTCAA	CAGGTGTAAA	ACAGACGTGA	CGTGGCAAAG	2880
CTT						2883

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2857 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTCCAGCGGT	ACCATGGGCC	GTCGGAGCGC	GCTACCCCTT	GCCGTGGTCT	CTGCCCTGCT	60
GTGCCAGGTC	TGGAGCTCCG	GCGTATTTGA	GCTGAAGCTG	CAGGAGTTCG	TCAACAAGAA	120
GGGGCTGCTG	GGGAACCGCA	ACTGCTGCCG	CGGGGGCTCT	GGCCCGCCTT	GCGCCTGCAG	180
GACCTTCTTT	CGCGTATGCC	TCAACCACTA	CCAGGCCAGC	GTGTCACCGG	AGCCACCCTG	240
CACCTACGGC	AGTGCTGTCA	CGCCAGTGCT	GGGTCTCGAC	TCCTTCAGCC	TGCCTGATGG	300
CGCAGGCATC	GACCCCGCCT	TCAGCAACCC	ATCCGATTCC	CCTTCCGGCT	TCACCTGGCC	360
AGGTACCTTC	TCTCTGATCA	TTGAAGCCCT	CCATACAGAC	TCTCCCGATG	ACCTCGCAAC	420
AGAAAACCCA	GAAAGACTCA	TCAGCCGCCT	GACCACACAG	AGGCACCTCA	CTGTGGGACG	480
AATGGTCTCA	GGACCTTCAC	AGTAGCGGCC	GCACAGACCT	CCGGTACTCT	TACCGGTTTG	540
TGTGTGACGA	GCACTACTAC	GGAGAAGGTT	GCTCTGTGTT	CTGCCGACCT	CGGGATGACG	600
CCTTTGGCCA	CTTCACCTGC	GGGGACAGAG	GGGAGAAGAT	GTGCGACCCT	GGCTGGAAAG	660
GCCAGTACTG	CACTGACCCA	ATCTGTCTGC	CAGGGTGTGA	TGACCAACAT	GGATACTGTG	720
ACAAACCAGG	GGAGTGCAAG	TGCAGAGTTG	GCTGGCAGGG	CCGCTACTGC	GATGAGTGCA	780
TCCGATACCC	AGGTTGTCTC	CATGGCACCT	GCCAGCAACC	CTGGCAGTGT	AACTGCCAGG	840
AAGGCTGGGG	GGGCCTTTTC	TGCAACCAAG	ACCTGAAC TA	CTGTACTCAC	CATAAGCCGT	900
GCAGGAATGG	AGCCACCTGC	ACCAACACGG	GCCAGGGGAG	CTACACATGT	TCCTGCCGAC	960
TGGGGTATAC	AGGTGCCAAC	TGTGAGCTGG	AAGTAGATGA	GTGTGCTCCT	AGCCCCTGCA	1020
AGAACGGAGC	GAGCTGCACG	GACCTTGAGG	ACAGCTTCTC	TTGCACCTGC	CCTCCCGGCT	1080
TCTATGGCAA	GGTCTGTGAG	CTTGAGCGCC	ATGACCTGTG	CAGATGGCCC	TTGCTTCAAT	1140
GGAGGACGAT	GTTCAAGATA	CCCTGACGGA	GGCTACACCT	GCCATTGCCC	CTTGGGCTTC	1200
TCTGGCTTCA	ACTGTGAGAA	GAAGATGGAT	CTCTGCGGCT	CTTCCCCCTT	GTTCTAACGG	1260

TGCCAAGTGT GTGGACCTCG GCAACTCTTA CCTGTGCCGG TGCCAGGCTG GCTTCTCCGG 1320
 GACCTACTGC GAGGACAATG TGGATGACTG TGCCTCCTCC CCGTGTGCAA ATGGGGGCAC 1380
 CTGCCGGGAC AGTGTGAACG ACTTCTCCTC TACCTGCCCA CCTGGCTACA CGGGCAAGAA 1440
 CTGCAGCGCC CCTGTCAGCA GGTGTGAGCA TGCACCCTGC CATAATGGGG CCACCTGCCA 1500
 CCAGAGGGGC CAGCGCTACA TGTGTGAGTG CGCCCAGGGC TATGGCGGGC CCAACTGCCA 1560
 GTTCTGCTC CCTGAGCCAC CACCAGGGCC CATGGTGGTG GACCTCAGTG AGAGGCATAT 1620
 GGAGAGCCAG GGCGGGCCCT TCCCCTCGGT GGCGGTGTGT GCCGGGGTGG TGCTTGTCCT 1680
 CCTGCTGCTG CTGGGCTGTG CTGCTGTGGT GGTCTGCGTC CGGCTGAAGC TACAGAAACA 1740
 CCAGCCTCCA CCTGAACCCT GTGGGGGAGA GACAGAAACC ATGAACAACC TAGCCAATTG 1800
 CCAGCGCGAG AAGGACGTTT CTGTTAGCAT CATTGGGGCT ACCCAGATCA AGAACACCAA 1860
 CAAGAAGGCG GACTTTCACG GGGACCATGG AGCCAAGAAG AGCAGCTTTA AGGTCCGATA 1920
 CCCCCTGTG GACTATAACC TCGTTCGAGA CCTCAAGGGA GATGAAGCCA CGGTCAGGGA 1980
 TACACACAGC AAACGTGACA CCAAGTGCCA GTCACAGAGC TCTGCAGGAG AAGAGAAGAT 2040
 CGCCCCAACA CTTAGGGGTG GGGAGATTCC TGACAGAAAA AGGCCAGAGT CTGTCTACTC 2100
 TACTTCAAAG GACACCAAGT ACCAGTCGGT GTATGTTCTG TCTGCAGAAA AGGATGAGTG 2160
 TGTTATAGCG ACTGAGCTGT AAGATGGAAG CGATGTGGCA AAATTCCCAT TTCTCTCAA 2220
 TAAATTTCCA AGGATATAGC CCCGATGAAT GCTGCTGAGA GAGGAAGGGA GAGGAAACCC 2280
 AGGGACTGCT GCTGAGAACC AGGTTTCAGGC GAAGCTGGTT CTCTCAGAGT TAGCAGAGGC 2340
 GCCCGACACT GCCAGCCTAG GCTTTGGCTG CCGCTGGACT GCCTGCTGGT TGTTCCTATT 2400
 GCACTATGGA CAGTTGCTTT GAAGAGTATA TATTTAAATG GACGAGTGAC TTGATTCATA 2460
 TACGAAGCAC GCACTGCCCA CACGTCTATC TTGGATTACT ATGAGCCAGT CTTTCCTTGA 2520
 ACTAGAAACA CAACTGCCTT TATTGTCCTT TTTGATACTG AGATGTGTTT TTTTTTTTCC 2580
 TAGACGGGAA AAAGAAAACG TGTGTTATTT TTTTGGGATT TGTAATAATA TTTTTCATGA 2640
 TATCTGTAAA GCTTGAGTAT TTTGTGACGT TCATTTTTTT ATAATTTAAA TTTTGGTAAA 2700
 TATGTACAAA GGCACCTCGG GTCTATGTGA CTATATTTTT TTGTATATAA ATGTATTTAT 2760
 GGAATATTGT GCAAATGTTA TTTGAGTTTT TTAAGTTTTT GTTAATGAAG AAATTCATTT 2820
 TAAAAATATT TTTCCAAAAT AAATATAATG AACTACA 2857

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Gly	Gln	Gln	Arg	Met	Leu	Thr	Leu	Leu	Val	Leu	Ser	Ala	Val	Leu
1				5				10						15	
Cys	Gln	Ile	Ser	Cys	Ser	Gly	Leu	Phe	Glu	Leu	Arg	Leu	Gln	Glu	Phe
			20					25					30		
Val	Asn	Lys	Lys	Gly	Leu	Leu	Gly	Asn	Met	Asn	Cys	Cys	Arg	Pro	Gly
		35					40					45			
Ser	Leu	Ala	Ser	Leu	Gln	Arg	Cys	Glu	Cys	Lys	Thr	Phe	Phe	Arg	Ile
		50				55					60				
Cys	Leu	Lys	His	Tyr	Gln	Ser	Asn	Val	Ser	Pro	Glu	Pro	Pro	Cys	Thr
65					70					75				80	
Tyr	Gly	Gly	Ala	Val	Thr	Pro	Val	Leu	Gly	Thr	Asn	Ser	Phe	Val	Val
			85					90						95	
Pro	Glu	Ser	Ser	Asn	Ala	Asp	Pro	Thr	Phe	Ser	Asn	Pro	Ile	Arg	Phe
			100					105					110		
Pro	Phe	Gly	Phe	Thr	Trp	Pro	Gly	Thr	Phe	Ser	Leu	Ile	Ile	Glu	Ala
		115					120					125			
Ile	His	Ala	Asp	Ser	Ala	Asp	Asp	Leu	Asn	Thr	Glu	Asn	Pro	Glu	Arg
		130				135					140				

Leu Ile Ser Arg Leu Ala Thr Gln Arg His Leu Thr Val Gly Glu Gln
 145 150 155 160
 Trp Ser Gln Asp Leu His Ser Ser Asp Arg Thr Glu Leu Lys Tyr Ser
 165 170 175
 Tyr Arg Phe Val Cys Asp Glu Tyr Tyr Tyr Gly Glu Gly Cys Ser Asp
 180 185 190
 Tyr Cys Arg Pro Arg Asp Asp Ala Phe Gly His Phe Ser Cys Gly Glu
 195 200 205
 Lys Gly Glu Lys Leu Cys Asn Pro Gly Trp Lys Gly Leu Tyr Cys Thr
 210 215 220
 Glu Pro Ile Cys Leu Pro Gly Cys Asp Glu His His Gly Tyr Cys Asp
 225 230 235 240
 Lys Pro Gly Glu Cys Lys Cys Arg Val Gly Trp Gln Gly Arg Tyr Cys
 245 250 255
 Asp Glu Cys Ile Arg Tyr Pro Gly Cys Leu His Gly Thr Cys Gln Gln
 260 265 270
 Pro Trp Gln Cys Asn Cys Gln Glu Gly Trp Gly Gly Leu Phe Cys Asn
 275 280 285
 Gln Asp Leu Asn Tyr Cys Thr His His Lys Pro Cys Glu Asn Gly Ala
 290 295 300
 Thr Cys Thr Asn Thr Gly Gln Gly Ser Tyr Thr Cys Ser Cys Arg Pro
 305 310 315 320
 Gly Tyr Thr Gly Ser Asn Cys Glu Ile Glu Val Asn Glu Cys Asp Ala
 325 330 335
 Asn Pro Cys Lys Asn Gly Gly Ser Cys Ser Asp Leu Glu Asn Ser Tyr
 340 345 350
 Thr Cys Ser Cys Pro Pro Gly Phe Tyr Gly Lys Asn Cys Glu Leu Ser
 355 360 365
 Ala Met Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Arg Cys Ala
 370 375 380
 Asp Asn Pro Asp Gly Gly Tyr Ile Cys Phe Cys Pro Val Gly Tyr Ser
 385 390 395 400
 Gly Phe Asn Cys Glu Lys Lys Ile Asp Tyr Cys Ser Ser Asn Pro Cys
 405 410 415
 Ala Asn Gly Ala Arg Cys Glu Asp Leu Gly Asn Ser Tyr Ile Cys Gln
 420 425 430
 Cys Gln Glu Gly Phe Ser Gly Arg Asn Cys Asp Asp Asn Leu Asp Asp
 435 440 445
 Cys Thr Ser Phe Pro Cys Gln Asn Gly Gly Thr Cys Gln Asp Gly Ile
 450 455 460
 Asn Asp Tyr Ser Cys Thr Cys Pro Pro Gly Tyr Ile Gly Lys Asn Cys
 465 470 475 480
 Ser Met Pro Ile Thr Lys Cys Glu His Asn Pro Cys His Asn Gly Ala
 485 490 495
 Thr Cys His Glu Arg Asn Asn Arg Tyr Val Cys Gln Cys Ala Arg Gly
 500 505 510
 Tyr Gly Gly Asn Asn Cys Gln Phe Leu Leu Pro Glu Glu Lys Pro Val
 515 520 525
 Val Val Asp Leu Thr Glu Lys Tyr Thr Glu Gly Gln Ser Gly Gln Phe
 530 535 540
 Pro Trp Ile Ala Val Cys Ala Gly Ile Val Leu Val Leu Met Leu Leu
 545 550 555 560
 Leu Gly Cys Ala Ala Val Val Val Cys Val Arg Val Arg Val Gln Lys
 565 570 575
 Arg Arg His Gln Pro Glu Ala Cys Arg Gly Glu Ser Lys Thr Met Asn
 580 585 590
 Asn Leu Ala Asn Cys Gln Arg Glu Lys Asp Ile Ser Val Ser Phe Ile
 595 600 605

Gly	Thr	Thr	Gln	Ile	Lys	Asn	Thr	Asn	Lys	Lys	Ile	Asp	Phe	Leu	Ser
610						615					620				
Glu	Ser	Asn	Asn	Glu	Lys	Asn	Gly	Tyr	Lys	Pro	Arg	Tyr	Pro	Ser	Val
625					630					635					640
Asp	Tyr	Asn	Leu	Val	His	Glu	Leu	Lys	Asn	Glu	Asp	Ser	Pro	Lys	Glu
				645					650					655	
Glu	Arg	Ser	Lys	Cys	Glu	Ala	Lys	Cys	Ser	Ser	Asn	Asp	Ser	Asp	Ser
			660					665					670		
Glu	Asp	Val	Asn	Ser	Val	His	Ser	Lys	Arg	Asp	Ser	Ser	Glu	Arg	Arg
		675					680					685			
Arg	Pro	Asp	Ser	Ala	Tyr	Ser	Thr	Ser	Lys	Asp	Thr	Lys	Tyr	Gln	Ser
	690					695					700				
Val	Tyr	Val	Ile	Ser	Asp	Glu	Lys	Asp	Glu	Cys	Ile	Ile	Ala	Thr	Glu
705					710					715					720
Val															

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	His	Trp	Ile	Lys	Cys	Leu	Leu	Thr	Ala	Phe	Ile	Cys	Phe	Thr	Val
1				5					10					15	
Ile	Val	Gln	Val	His	Ser	Ser	Gly	Ser	Phe	Glu	Leu	Arg	Leu	Lys	Tyr
			20					25					30		
Phe	Ser	Asn	Asp	His	Gly	Arg	Asp	Asn	Glu	Gly	Arg	Cys	Cys	Ser	Gly
		35					40					45			
Glu	Ser	Asp	Gly	Ala	Thr	Gly	Lys	Cys	Leu	Gly	Ser	Cys	Lys	Thr	Arg
	50					55					60				
Phe	Arg	Leu	Cys	Leu	Lys	His	Tyr	Gln	Ala	Thr	Ile	Asp	Thr	Thr	Ser
65					70					75					80
Gln	Cys	Thr	Tyr	Gly	Asp	Val	Ile	Thr	Pro	Ile	Leu	Gly	Glu	Asn	Ser
				85					90					95	
Val	Asn	Leu	Thr	Asp	Ala	Gln	Arg	Phe	Gln	Asn	Lys	Gly	Phe	Thr	Asn
			100					105					110		
Pro	Ile	Gln	Phe	Pro	Phe	Ser	Phe	Ser	Trp	Pro	Gly	Thr	Phe	Ser	Leu
		115					120					125			
Ile	Val	Glu	Ala	Trp	His	Asp	Thr	Asn	Asn	Ser	Gly	Asn	Ala	Arg	Thr
	130					135						140			
Asn	Lys	Leu	Leu	Ile	Gln	Arg	Leu	Leu	Val	Gln	Gln	Val	Leu	Glu	Val
145					150					155					160
Ser	Ser	Glu	Trp	Lys	Thr	Asn	Lys	Ser	Glu	Ser	Gln	Tyr	Thr	Ser	Leu
				165					170					175	
Glu	Tyr	Asp	Phe	Arg	Val	Thr	Cys	Asp	Leu	Asn	Tyr	Tyr	Gly	Ser	Gly
		180						185					190		
Cys	Ala	Lys	Phe	Cys	Arg	Pro	Arg	Asp	Asp	Ser	Phe	Gly	His	Ser	Thr
		195					200					205			
Cys	Ser	Glu	Thr	Gly	Glu	Ile	Ile	Cys	Leu	Thr	Gly	Trp	Gln	Gly	Asp
210						215						220			

Tyr	Cys	His	Ile	Pro	Lys	Cys	Ala	Lys	Gly	Cys	Glu	His	Gly	His	Cys	
225					230					235					240	
Asp	Lys	Pro	Asn	Gln	Cys	Val	Cys	Gln	Leu	Gly	Trp	Lys	Gly	Ala	Leu	
				245					250					255		
Cys	Asn	Glu	Cys	Val	Leu	Glu	Pro	Asn	Cys	Ile	His	Gly	Thr	Cys	Asn	
			260					265					270			
Lys	Pro	Trp	Thr	Cys	Ile	Cys	Asn	Glu	Gly	Trp	Gly	Gly	Leu	Tyr	Cys	
		275					280					285				
Asn	Gln	Asp	Leu	Asn	Tyr	Cys	Thr	Asn	His	Arg	Pro	Cys	Lys	Asn	Gly	
	290					295					300					
Gly	Thr	Cys	Phe	Asn	Thr	Gly	Glu	Gly	Leu	Tyr	Thr	Cys	Lys	Cys	Ala	
305					310					315					320	
Pro	Gly	Tyr	Ser	Gly	Asp	Asp	Cys	Glu	Asn	Glu	Ile	Tyr	Ser	Cys	Asp	
				325					330					335		
Ala	Asp	Val	Asn	Pro	Cys	Gln	Asn	Gly	Gly	Thr	Cys	Ile	Asp	Glu	Pro	
			340					345					350			
His	Thr	Lys	Thr	Gly	Tyr	Lys	Cys	His	Cys	Arg	Asn	Gly	Trp	Ser	Gly	
		355					360					365				
Lys	Met	Cys	Glu	Glu	Lys	Val	Leu	Thr	Cys	Ser	Asp	Lys	Pro	Cys	His	
	370					375					380					
Gln	Gly	Ile	Cys	Arg	Asn	Val	Arg	Pro	Gly	Leu	Gly	Ser	Lys	Gly	Gln	
385					390					395					400	
Gly	Tyr	Gln	Cys	Glu	Cys	Pro	Ile	Gly	Tyr	Ser	Gly	Pro	Asn	Cys	Asp	
				405					410					415		
Leu	Gln	Leu	Asp	Asn	Cys	Ser	Pro	Asn	Pro	Cys	Ile	Asn	Gly	Gly	Ser	
			420					425					430			
Cys	Gln	Pro	Ser	Gly	Lys	Cys	Ile	Cys	Pro	Ser	Gly	Phe	Ser	Gly	Thr	
		435					440					445				
Arg	Cys	Glu	Thr	Asn	Ile	Asp	Asp	Cys	Leu	Gly	His	Gln	Cys	Glu	Asn	
	450					455					460					
Gly	Gly	Thr	Cys	Ile	Asp	Met	Val	Asn	Gln	Tyr	Arg	Cys	Gln	Cys	Val	
465					470					475					480	
Pro	Gly	Phe	His	Gly	Thr	His	Cys	Ser	Ser	Lys	Val	Asp	Leu	Cys	Leu	
				485					490					495		
Ile	Arg	Pro	Cys	Ala	Asn	Gly	Gly	Thr	Cys	Leu	Asn	Leu	Asn	Asn	Asp	
			500					505					510			
Tyr	Gln	Cys	Thr	Cys	Arg	Ala	Gly	Phe	Thr	Gly	Lys	Asp	Cys	Ser	Val	
		515					520					525				
Asp	Ile	Asp	Glu	Cys	Ser	Ser	Gly	Pro	Cys	His	Asn	Gly	Gly	Thr	Cys	
	530					535					540					
Met	Asn	Arg	Val	Asn	Ser	Phe	Glu	Cys	Val	Cys	Ala	Asn	Gly	Phe	Arg	
545					550					555					560	
Gly	Lys	Gln	Cys	Asp	Glu	Glu	Ser	Tyr	Asp	Ser	Val	Thr	Phe	Asp	Ala	
				565					570					575		
His	Gln	Tyr	Gly	Ala	Thr	Thr	Gln	Ala	Arg	Ala	Asp	Gly	Leu	Ala	Asn	
			580					585					590			
Ala	Gln	Val	Val	Leu	Ile	Ala	Val	Phe	Ser	Val	Ala	Met	Pro	Leu	Val	
		595					600					605				
Ala	Val	Ile	Ala	Ala	Cys	Val	Val	Phe	Cys	Met	Lys	Arg	Lys	Arg	Lys	
						615					620					
Arg	Ala	Gln	Glu	Lys	Asp	Asn	Ala	Glu	Ala	Arg	Lys	Gln	Asn	Glu	Gln	
625					630					635					640	
Asn	Ala	Val	Ala	Thr	Met	His	His	Asn	Gly	Ser	Ala	Val	Gly	Val	Ala	
				645					650					655		
Leu	Ala	Ser	Ala	Ser	Met	Gly	Gly	Lys	Thr	Gly	Ser	Asn	Ser	Gly	Leu	
			660					665					670			
Thr	Phe	Asp	Gly	Gly	Asn	Pro	Asn	Ile	Ile	Lys	Asn	Thr	Trp	Asp	Lys	
		675					680					685				

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Ser Val Asn Asn Ile Cys Ala Ser Ala Ala Ala Ala Ala Ala Ala
690 695 700
Ala Ala Ala Asp Glu Cys Leu Met Tyr Gly Gly Tyr Val Ala Ser Val
705 710 715 720
Ala Asp Asn Asn Asn Ala Asn Ser Asp Phe Cys Val Ala Pro Leu Gln
725 730 735
Arg Ala Lys Ser Gln Lys Gln Leu Asn Thr Asp Pro Thr Leu Met His
740 745 750
Arg Gly Ser Pro Ala Gly Thr Ser Ala Lys Gly Ala Ser Gly Gly Gly
755 760 765
Pro Gly Ala Ala Glu Gly Lys Arg Ile Ser Val Leu Gly Glu Gly Ser
770 775 780
Tyr Cys Ser Gln Arg Trp Pro Ser Leu Ala Ala Gly Val Ala Gly
785 790 795 800
Asp Leu Phe Ile Gln Leu Met Ala Ala Ala Ser Val Ala Gly Thr Asp
805 810 815
Gly Thr Ala Gln Gln Gln Arg Ser Val Val Cys Gly Thr Pro His Met
820 825 830

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Val Gln Cys Ala Val Thr Tyr Tyr Asn Thr Thr Phe Cys Thr Thr Phe
1 5 10 15
Cys Arg Pro Arg Asp Asp Gln Phe Gly His Tyr Ala Cys Gly Ser Glu
20 25 30
Gly Gln Lys Leu Cys Leu Asn Gly Trp Gln Gly Val Asn Cys
35 40 45

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Val Thr Cys Ala Glu His Tyr Tyr Gly Phe Gly Cys Asn Lys Phe Cys
1 5 10 15
Arg Pro Arg Asp Asp Phe Phe Thr His His Thr Cys Asp Gln Asn Gly
20 25 30
Asn Lys Thr Cys Leu Glu Gly Trp Thr Gly Pro Glu Cys
35 40 45

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asn Leu Cys Ser Ser Asn Tyr His Gly Lys Arg Cys Asn Arg Tyr Cys
1 5 10 15
Ile Ala Asn Ala Lys Leu His Trp Glu Cys Ser Thr His Gly Val Arg
20 25 30
Arg Cys Ser Ala Gly Trp Ser Gly Glu Asp Cys
35 40

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Val Thr Cys Ala Arg Asn Tyr Phe Gly Asn Arg Cys Glu Asn Phe Cys
1 5 10 15
Asp Ala His Leu Ala Lys Ala Ala Arg Lys Arg Cys Asp Ala Met Gly
20 25 30
Arg Leu Arg Cys Asp Ile Gly Trp Met Gly Pro His Cys
35 40 45

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...2199
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTGCAGGAAT TCSMYCGCAT GCTCCCGGCC GCC ATG GGC CGT CGG AGC GCG CTA
Met Gly Arg Arg Ser Ala Leu
1 5

54

GCC CTT GCC GTG GTC TCT GCC CTG CTG TGC CAG GTC TGG AGC TCC GGC	102
Ala Leu Ala Val Val Ser Ala Leu Leu Cys Gln Val Trp Ser Ser Gly	
10 15 20	
GTA TTT GAG CTG AAG CTG CAG GAG TTC GTC AAC AAG AAG GGG CTG CTG	150
Val Phe Glu Leu Lys Leu Gln Glu Phe Val Asn Lys Lys Gly Leu Leu	
25 30 35	
GGG AAC CGC AAC TGC TGC CGC GGG GGC TCT GGC CCG CCT TGC GCC TGC	198
Gly Asn Arg Asn Cys Cys Arg Gly Gly Ser Gly Pro Pro Cys Ala Cys	
40 45 50 55	
AGG ACC TTC TTT CGC GTA TGC CTC AAG CAC TAC CAG GCC AGC GTG TCA	246
Arg Thr Phe Phe Arg Val Cys Leu Lys His Tyr Gln Ala Ser Val Ser	
60 65 70	
CCG GAG CCA CCC TGC ACC TAC GGC AGT GCC GTC ACG CCA GTG CTG GGT	294
Pro Glu Pro Pro Cys Thr Tyr Gly Ser Ala Val Thr Pro Val Leu Gly	
75 80 85	
GTC GAC TCC TTC AGC CTG CCT GAT GGC GCA GGC ATC GAC CCC GCC TTC	342
Val Asp Ser Phe Ser Leu Pro Asp Gly Ala Gly Ile Asp Pro Ala Phe	
90 95 100	
AGC AAC CCC ATC CGA TTC CCC TTC GGC TTC ACC TGG CCA GGT ACC TTC	390
Ser Asn Pro Ile Arg Phe Pro Phe Gly Phe Thr Trp Pro Gly Thr Phe	
105 110 115	
TCT CTG ATC ATT GAA GCC CTC CAT ACA GAC TCT CCC GAT GAC CTC GCA	438
Ser Leu Ile Ile Glu Ala Leu His Thr Asp Ser Pro Asp Asp Leu Ala	
120 125 130 135	
ACA GAA AAC CCA GAA AGA CTC ATC AGC CGC CTG ACC ACA CAG AGG CAC	486
Thr Glu Asn Pro Glu Arg Leu Ile Ser Arg Leu Thr Thr Gln Arg His	
140 145 150	
CTC ACT GTG GGA GAA GAA TGG TCT CAG GAC CTT CAC AGT AGC GGC CGC	534
Leu Thr Val Gly Glu Glu Trp Ser Gln Asp Leu His Ser Ser Gly Arg	
155 160 165	
ACA GAC CTC CGG TAC TCT TAC CGG TTT GTG TGT GAC GAG CAC TAC TAC	582
Thr Asp Leu Arg Tyr Ser Tyr Arg Phe Val Cys Asp Glu His Tyr Tyr	
170 175 180	
GGA GAA GGT TGC TCT GTG TTC TGC CGA CCT CGG GAT GAC GCC TTT GGC	630
Gly Glu Gly Cys Ser Val Phe Cys Arg Pro Arg Asp Asp Ala Phe Gly	
185 190 195	
CAC TTC ACC TGC GGG GAC AGA GGG GAG AAG ATG TGC GAC CCT GGC TGG	678
His Phe Thr Cys Gly Asp Arg Gly Glu Lys Met Cys Asp Pro Gly Trp	
200 205 210 215	
AAA GGC CAG TAC TGC ACT GAC CCA ATC TGT CTG CCA GGG TGT GAT GAC	726
Lys Gly Gln Tyr Cys Thr Asp Pro Ile Cys Leu Pro Gly Cys Asp Asp	
220 225 230	

CAA CAT GGA TAC TGT GAC AAA CCA GGG GAG TGC AAG TGC AGA GTT GGC	774
Gln His Gly Tyr Cys Asp Lys Pro Gly Glu Cys Lys Cys Arg Val Gly	
235 240 245	
TGG CAG GGC CGC TAC TGC GAT GAG TGC ATC CGA TAC CCA GGT TGT GTC	822
Trp Gln Gly Arg Tyr Cys Asp Glu Cys Ile Arg Tyr Pro Gly Cys Val	
250 255 260	
CAT GGC ACC TGC CAG CAA CCC TGG CAG TGT AAC TGC CAG GAA GGC TGG	870
His Gly Thr Cys Gln Gln Pro Trp Gln Cys Asn Cys Gln Glu Gly Trp	
265 270 275	
GGG GGC CTT TTC TGC AAC CAA GAC CTG AAC TAC TGT ACT CAC CAT AAG	918
Gly Gly Leu Phe Cys Asn Gln Asp Leu Asn Tyr Cys Thr His His Lys	
280 285 290 295	
CCG TGC AGG AAT GGA GCC ACC TGC ACC AAC ACG GGC CAG GGG AGC TAC	966
Pro Cys Arg Asn Gly Ala Thr Cys Thr Asn Thr Gly Gln Gly Ser Tyr	
300 305 310	
ACA TGT TCC TGC CGA CCT GGG TAT ACA GGT GCC AAC TGT GAG CTG GAA	1014
Thr Cys Ser Cys Arg Pro Gly Tyr Thr Gly Ala Asn Cys Glu Leu Glu	
315 320 325	
GTA GAT GAG TGT GCT CCT AGC CCC TGC AAG AAC GGA GCG AGC TGC ACG	1062
Val Asp Glu Cys Ala Pro Ser Pro Cys Lys Asn Gly Ala Ser Cys Thr	
330 335 340	
GAC CTT GAG GAC AGC TTC TCT TGC ACC TGC CCT CCC GGC TTC TAT GGC	1110
Asp Leu Glu Asp Ser Phe Ser Cys Thr Cys Pro Pro Gly Phe Tyr Gly	
345 350 355	
AAG GTC TGT GAG CTG AGC GCC ATG ACC TGT GCA GAT GGC CCT TGC TTC	1158
Lys Val Cys Glu Leu Ser Ala Met Thr Cys Ala Asp Gly Pro Cys Phe	
360 365 370 375	
AAT GGA GGA CGA TGT TCA GAT AAC CCT GAC GGA GGC TAC ACC TGC CAT	1206
Asn Gly Gly Arg Cys Ser Asp Asn Pro Asp Gly Gly Tyr Thr Cys His	
380 385 390	
TGC CCC TTG GGC TTC TCT GGC TTC AAC TGT GAG AAG AAG ATG GAT CTC	1254
Cys Pro Leu Gly Phe Ser Gly Phe Asn Cys Glu Lys Lys Met Asp Leu	
395 400 405	
TGC GGC TCT TCC CCT TGT TCT AAC GGT GCC AAG TGT GTG GAC CTC GGC	1302
Cys Gly Ser Ser Pro Cys Ser Asn Gly Ala Lys Cys Val Asp Leu Gly	
410 415 420	
AAC TCT TAC CTG TGC CGG TGC CAG GCT GGC TTC TCC GGG AGG TAC TGC	1350
Asn Ser Tyr Leu Cys Arg Cys Gln Ala Gly Phe Ser Gly Arg Tyr Cys	
425 430 435	
GAG GAC AAT GTG GAT GAC TGT GCC TCC TCC CCG TGT GCA AAT GGG GGC	1398
Glu Asp Asn Val Asp Asp Cys Ala Ser Ser Pro Cys Ala Asn Gly Gly	
440 445 450 455	

ACC TGC CGG GAC AGT GTG AAC GAC TTC TCC TGT ACC TGC CCA CCT GGC	1446
Thr Cys Arg Asp Ser Val Asn Asp Phe Ser Cys Thr Cys Pro Pro Gly	
460 465 470	
TAC ACG GGC AAG AAC TGC AGC GCC CCT GTC AGC AGG TGT GAG CAT GCA	1494
Tyr Thr Gly Lys Asn Cys Ser Ala Pro Val Ser Arg Cys Glu His Ala	
475 480 485	
CCC TGC CAT AAT GGG GCC ACC TGC CAC CAG AGG GGC CAG CGC TAC ATG	1542
Pro Cys His Asn Gly Ala Thr Cys His Gln Arg Gly Gln Arg Tyr Met	
490 495 500	
TGT GAG TGC GCC CAG GGC TAT GGC GGC CCC AAC TGC CAG TTT CTG CTC	1590
Cys Glu Cys Ala Gln Gly Tyr Gly Gly Pro Asn Cys Gln Phe Leu Leu	
505 510 515	
CCT GAG CCA CCA CCA GGG CCC ATG GTG GTG GAC CTC AGT GAG AGG CAT	1638
Pro Glu Pro Pro Pro Gly Pro Met Val Val Asp Leu Ser Glu Arg His	
520 525 530 535	
ATG GAG AGC CAG GGC GGG CCC TTC CCC TGG GTG GCC GTG TGT GCC GGG	1686
Met Glu Ser Gln Gly Gly Pro Phe Pro Trp Val Ala Val Cys Ala Gly	
540 545 550	
GTG GTG CTT GTC CTC CTG CTG CTG CTG GGC TGT GCT GCT GTG GTG GTC	1734
Val Val Leu Val Leu Leu Leu Leu Leu Gly Cys Ala Ala Val Val Val	
555 560 565	
TGC GTC CGG CTG AAG CTA CAG AAA CAC CAG CCT CCA CCT GAA CCC TGT	1782
Cys Val Arg Leu Lys Leu Gln Lys His Gln Pro Pro Pro Glu Pro Cys	
570 575 580	
GGG GGA GAG ACA GAA ACC ATG AAC AAC CTA GCC AAT TGC CAG CGC GAG	1830
Gly Gly Glu Thr Glu Thr Met Asn Asn Leu Ala Asn Cys Gln Arg Glu	
585 590 595	
AAG GAC GTT TCT GTT AGC ATC ATT GGG GCT ACC CAG ATC AAG AAC ACC	1878
Lys Asp Val Ser Val Ser Ile Ile Gly Ala Thr Gln Ile Lys Asn Thr	
600 605 610 615	
AAC AAG AAG GCG GAC TTT CAC GGG GAC CAT GGA GCC GAG AAG AGC AGC	1926
Asn Lys Lys Ala Asp Phe His Gly Asp His Gly Ala Glu Lys Ser Ser	
620 625 630	
TTT AAG GTC CGA TAC CCC ACT GTG GAC TAT AAC CTC GTT CGA GAC CTC	1974
Phe Lys Val Arg Tyr Pro Thr Val Asp Tyr Asn Leu Val Arg Asp Leu	
635 640 645	
AAG GGA GAT GAA GCC ACG GTC AGG GAT ACA CAC AGC AAA CGT GAC ACC	2022
Lys Gly Asp Glu Ala Thr Val Arg Asp Thr His Ser Lys Arg Asp Thr	
650 655 660	
AAG TGC CAG TCA CAG AGT CTG CAG GAG AAG AGA AGA TCG CCC CAA CAC	2070
Lys Cys Gln Ser Gln Ser Leu Gln Glu Lys Arg Arg Ser Pro Gln His	
665 670 675	

TTA GGG GTG GGG AGA TTC CTG ACA GAA AAC AGG CCA GAG TCT GTC TAC	2118
Leu Gly Val Gly Arg Phe Leu Thr Glu Asn Arg Pro Glu Ser Val Tyr	
680 685 690 695	
TCT ACT TCA AAG GAC ACC AAG TAC CAG TCG GTG TAT GTT CTG TCT GCA	2166
Ser Thr Ser Lys Asp Thr Lys Tyr Gln Ser Val Tyr Val Leu Ser Ala	
700 705 710	
GAA AAG GAT GAG TGT GTT ATA GCG ACT GAG GTG TAAGATGGAA GCGATGTGGC	2219
Glu Lys Asp Glu Cys Val Ile Ala Thr Glu Val	
715 720	
AAAATTCCCA TTTCTCTTAA ATAAAATTCC AAGGATATAG CCCCATGAA TGCTGCTGAG	2279
AGAGGAAGGG AGAGGAAACC CAGGGACTGC TGCTGAGAAC CAGGTTTCAGG CGAACGTGGT	2339
TCTCTCAGAG TTAGCAGAGG CGCCCGACAC TGCCAGCCTA GGCTTTGGCT GCCGCTGGAC	2399
TGCCTGCTGG TTGTTCCCAT TGCACATATGG ACAGTTGCTT TGAAGAGTAT ATATTTAAAT	2459
GGACGAGTGA CTTGATTCAT ATAGGAAGCA CGCACTGCCC ACACGTCTAT CTTGGATTAC	2519
TATGAGCCAG TCTTTCCTTG AACTAGAAAC ACAACTGCCT TTATTGTCCT TTTTGATACT	2579
GAGATGTGTT TTTTTTTTTT CCTAGACGGG AAAAAGAAAA CGTGTGTTAT TTTTTTTGGG	2639
ATTTGTAAAA ATATTTTTC A TGATTATGGG AGAGCTCCCA ACGCGTTGGA GGT	2692

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Gly Arg Arg Ser Ala Leu Ala Leu Ala Val Val Ser Ala Leu Leu	
1 5 10 15	
Cys Gln Val Trp Ser Ser Gly Val Phe Glu Leu Lys Leu Gln Glu Phe	
20 25 30	
Val Asn Lys Lys Gly Leu Leu Gly Asn Arg Asn Cys Cys Arg Gly Gly	
35 40 45	
Ser Gly Pro Pro Cys Ala Cys Arg Thr Phe Phe Arg Val Cys Leu Lys	
50 55 60	
His Tyr Gln Ala Ser Val Ser Pro Glu Pro Pro Cys Thr Tyr Gly Ser	
65 70 75 80	
Ala Val Thr Pro Val Leu Gly Val Asp Ser Phe Ser Leu Pro Asp Gly	
85 90 95	
Ala Gly Ile Asp Pro Ala Phe Ser Asn Pro Ile Arg Phe Pro Phe Gly	
100 105 110	
Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Ala Leu His Thr	
115 120 125	
Asp Ser Pro Asp Asp Leu Ala Thr Glu Asn Pro Glu Arg Leu Ile Ser	
130 135 140	
Arg Leu Thr Thr Gln Arg His Leu Thr Val Gly Glu Glu Trp Ser Gln	
145 150 155 160	
Asp Leu His Ser Ser Gly Arg Thr Asp Leu Arg Tyr Ser Tyr Arg Phe	
165 170 175	
Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys Arg	
180 185 190	

Pro Arg Asp Asp Ala Phe Gly His Phe Thr Cys Gly Asp Arg Gly Glu
 195 200 205
 Lys Met Cys Asp Pro Gly Trp Lys Gly Gln Tyr Cys Thr Asp Pro Ile
 210 215 220
 Cys Leu Pro Gly Cys Asp Asp Gln His Gly Tyr Cys Asp Lys Pro Gly
 225 230 235 240
 Glu Cys Lys Cys Arg Val Gly Trp Gln Gly Arg Tyr Cys Asp Glu Cys
 245 250 255
 Ile Arg Tyr Pro Gly Cys Val His Gly Thr Cys Gln Gln Pro Trp Gln
 260 265 270
 Cys Asn Cys Gln Glu Gly Trp Gly Gly Leu Phe Cys Asn Gln Asp Leu
 275 280 285
 Asn Tyr Cys Thr His His Lys Pro Cys Arg Asn Gly Ala Thr Cys Thr
 290 295 300
 Asn Thr Gly Gln Gly Ser Tyr Thr Cys Ser Cys Arg Pro Gly Tyr Thr
 305 310 315 320
 Gly Ala Asn Cys Glu Leu Glu Val Asp Glu Cys Ala Pro Ser Pro Cys
 325 330 335
 Lys Asn Gly Ala Ser Cys Thr Asp Leu Glu Asp Ser Phe Ser Cys Thr
 340 345 350
 Cys Pro Pro Gly Phe Tyr Gly Lys Val Cys Glu Leu Ser Ala Met Thr
 355 360 365
 Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Arg Cys Ser Asp Asn Pro
 370 375 380
 Asp Gly Gly Tyr Thr Cys His Cys Pro Leu Gly Phe Ser Gly Phe Asn
 385 390 395 400
 Cys Glu Lys Lys Met Asp Leu Cys Gly Ser Ser Pro Cys Ser Asn Gly
 405 410 415
 Ala Lys Cys Val Asp Leu Gly Asn Ser Tyr Leu Cys Arg Cys Gln Ala
 420 425 430
 Gly Phe Ser Gly Arg Tyr Cys Glu Asp Asn Val Asp Asp Cys Ala Ser
 435 440 445
 Ser Pro Cys Ala Asn Gly Gly Thr Cys Arg Asp Ser Val Asn Asp Phe
 450 455 460
 Ser Cys Thr Cys Pro Pro Gly Tyr Thr Gly Lys Asn Cys Ser Ala Pro
 465 470 475 480
 Val Ser Arg Cys Glu His Ala Pro Cys His Asn Gly Ala Thr Cys His
 485 490 495
 Gln Arg Gly Gln Arg Tyr Met Cys Glu Cys Ala Gln Gly Tyr Gly Gly
 500 505 510
 Pro Asn Cys Gln Phe Leu Leu Pro Glu Pro Pro Pro Gly Pro Met Val
 515 520 525
 Val Asp Leu Ser Glu Arg His Met Glu Ser Gln Gly Gly Pro Phe Pro
 530 535 540
 Trp Val Ala Val Cys Ala Gly Val Val Leu Val Leu Leu Leu Leu
 545 550 555 560
 Gly Cys Ala Ala Val Val Cys Val Arg Leu Lys Leu Gln Lys His
 565 570 575
 Gln Pro Pro Pro Glu Pro Cys Gly Gly Glu Thr Glu Thr Met Asn Asn
 580 585 590
 Leu Ala Asn Cys Gln Arg Glu Lys Asp Val Ser Val Ser Ile Ile Gly
 595 600 605
 Ala Thr Gln Ile Lys Asn Thr Asn Lys Lys Ala Asp Phe His Gly Asp
 610 615 620
 His Gly Ala Glu Lys Ser Ser Phe Lys Val Arg Tyr Pro Thr Val Asp
 625 630 635 640
 Tyr Asn Leu Val Arg Asp Leu Lys Gly Asp Glu Ala Thr Val Arg Asp
 645 650 655

Thr	His	Ser	Lys	Arg	Asp	Thr	Lys	Cys	Gln	Ser	Gln	Ser	Leu	Gln	Glu
			660					665					670		
Lys	Arg	Arg	Ser	Pro	Gln	His	Leu	Gly	Val	Gly	Arg	Phe	Leu	Thr	Glu
		675					680					685			
Asn	Arg	Pro	Glu	Ser	Val	Tyr	Ser	Thr	Ser	Lys	Asp	Thr	Lys	Tyr	Gln
	690					695					700				
Ser	Val	Tyr	Val	Leu	Ser	Ala	Glu	Lys	Asp	Glu	Cys	Val	Ile	Ala	Thr
705					710					715					720
Glu	Val														

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Gly	Arg	Leu	Leu	Ala	Ser	Ala	Leu	Leu	Cys	Val	Ser	Gly	Val	Phe
1				5					10					15	
Glu	Leu	Lys	Leu	Gln	Glu	Phe	Val	Asn	Lys	Lys	Gly	Leu	Leu	Asn	Arg
			20					25					30		
Asn	Cys	Cys	Arg	Gly	Gly	Gly	Cys	Cys	Thr	Phe	Phe	Arg	Val	Cys	Leu
		35					40					45			
Lys	His	Tyr	Gln	Ala	Ser	Val	Ser	Pro	Glu	Pro	Pro	Cys	Thr	Tyr	Gly
	50					55					60				
Ser	Ala	Thr	Pro	Val	Leu	Gly	Ser	Phe	Ser	Pro	Asp	Gly	Ala	Gly	Asp
65					70					75					80
Pro	Ala	Phe	Ser	Asn	Pro	Ile	Arg	Phe	Pro	Phe	Gly	Phe	Thr	Trp	Pro
				85					90					95	
Gly	Thr	Phe	Ser	Leu	Ile	Ile	Glu	Ala	Leu	His	Thr	Asp	Ser	Pro	Asp
			100					105					110		
Asp	Leu	Thr	Glu	Asn	Pro	Glu	Arg	Leu	Ile	Ser	Arg	Leu	Thr	Gln	Arg
		115					120					125			
His	Leu	Val	Gly	Glu	Glu	Trp	Ser	Gln	Asp	Leu	His	Ser	Ser	Gly	Arg
	130					135					140				
Thr	Asp	Leu	Tyr	Ser	Tyr	Arg	Phe	Val	Cys	Asp	Glu	His	Tyr	Tyr	Gly
145					150					155					160
Glu	Gly	Cys	Ser	Val	Phe	Cys	Arg	Pro	Arg	Asp	Asp	Phe	Gly	His	Phe
			165						170					175	
Thr	Cys	Gly	Arg	Gly	Glu	Lys	Cys	Pro	Gly	Trp	Lys	Gly	Gln	Tyr	Cys
			180					185					190		
Thr	Pro	Ile	Cys	Leu	Pro	Gly	Cys	Asp	Gln	His	Gly	Cys	Asp	Lys	Pro
		195					200						205		
Gly	Glu	Cys	Lys	Cys	Arg	Val	Gly	Trp	Gln	Gly	Arg	Tyr	Cys	Asp	Glu
	210					215					220				
Cys	Ile	Arg	Tyr	Pro	Gly	Cys	Val	His	Gly	Thr	Cys	Gln	Gln	Pro	Trp
225					230					235					240
Gln	Cys	Asn	Cys	Gln	Glu	Gly	Trp	Gly	Gly	Leu	Phe	Cys	Asn	Gln	Asp
			245						250					255	
Leu	Asn	Tyr	Cys	Thr	His	His	Lys	Pro	Cys	Asn	Gly	Ala	Thr	Cys	Thr
			260					265						270	

Asn Thr Gly Gln Gly Ser Tyr Thr Cys Ser Cys Arg Pro Gly Tyr Thr
 275 280 285
 Gly Cys Glu Glu Glu Cys Pro Cys Lys Asn Gly Ser Cys Thr Asp Leu
 290 295 300
 Glu Ser Ser Cys Thr Cys Pro Pro Gly Phe Tyr Gly Lys Cys Glu Leu
 305 310 315 320
 Ser Ala Met Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Arg Cys
 325 330 335
 Asp Asn Pro Asp Gly Gly Tyr Cys Cys Pro Leu Gly Ser Gly Phe Asn
 340 345 350
 Cys Glu Lys Lys Asp Cys Ser Ser Pro Cys Asn Gly Ala Cys Val Asp
 355 360 365
 Leu Gly Asn Ser Tyr Cys Cys Gln Ala Gly Phe Gly Arg Cys Asp Asn
 370 375 380
 Val Asp Asp Cys Ala Ser Pro Cys Asn Gly Gly Thr Cys Asp Val Asn
 385 390 395 400
 Asp Ser Cys Thr Cys Pro Pro Gly Tyr Gly Lys Asn Cys Ser Pro Val
 405 410 415
 Ser Arg Cys Glu His Pro Cys His Asn Gly Ala Thr Cys His Arg Arg
 420 425 430
 Tyr Cys Glu Cys Ala Gly Tyr Gly Gly Asn Cys Gln Phe Leu Leu Pro
 435 440 445
 Glu Pro Pro Gly Pro Val Asp Glu Glu Gln Phe Pro Trp Ala Val Cys
 450 455 460
 Ala Gly Leu Val Leu Leu Leu Leu Gly Cys Ala Ala Val Val Cys Val
 465 470 475 480
 Arg Leu Lys Gln Lys Pro Glu Cys Glu Thr Glu Thr Met Asn Asn Leu
 485 490 495
 Ala Asn Cys Gln Arg Glu Lys Asp Ser Ser Ile Gly Ala Thr Gln Ile
 500 505 510
 Lys Asn Thr Asn Lys Lys Asp Phe His Asp Lys Lys Val Arg Tyr Pro
 515 520 525
 Val Asp Tyr Asn Leu Val Leu Lys Val His Lys Lys Cys Ser Glu Glu
 530 535 540
 Lys Ala Leu Arg Lys Arg Pro Ser Val Tyr Ser Thr Ser Lys Asp Thr
 545 550 555 560
 Lys Tyr Gln Ser Val Tyr Val Ser Glu Lys Asp Glu Cys Ile Ala Thr
 565 570 575
 Glu Val

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TACGATGAAY	AACCTGGCGA	ACTGCCAGCG	TGAGAAGGAC	ATCTCAGTCA	GCATCATCGG	60
GGCYACGTCA	GATCARGAAC	ACCAACAAGA	AGGCGGACTT	YMCASCGGGG	GACCASAGCG	120
TCCGACAAGA	ATGGMTTTC	AGGCCCGCTA	CCCCAGCGTG	GACTATAACT	CGTGCAGGAC	180
CTCAAGGGTG	ACGACACCGC	CGTCAGGACG	TCGCACAGCA	AGCGTGACAC	CAAGTGCCAG	240

TCCCCAGGCT	CCTCAGGGAG	GAGAAGGGGA	CCCCGACCAC	ACTCAGGGGK	TGCGTGCTGC	300
GGGCCGGGCT	CAGGAGGGGG	TACCTGGGGG	GTGTCTTCCT	GGAACCACTG	CTCCGTTTCT	360
CTTCCCAAAT	GTTCTCATGC	ATTCATTGTG	GATTTTCTCT	ATTTTCCTTT	TAGTGGAGAA	420
GCATCTGAAA	GAAAAAGGCC	GGACTCGGGC	TGTTCAACTT	CAAAAGACAC	CAAGTACCAG	480
TCGGTGTACG	TCATATCCGA	GGAGAAGGAC	GAGTGCGTCA	TCGCA		525

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Tyr	Asp	Glu	Xaa	Pro	Gly	Glu	Leu	Pro	Ala
1				5				10	

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu	Gly	His	Leu	Ser	Gln	His	His	Arg	Gly	Xaa	Val	Arg	Ser	Xaa	Thr
1				5					10					15	
Pro	Thr	Arg	Arg	Arg	Thr	Xaa	Xaa	Arg	Gly	Thr	Xaa	Ala	Ser	Asp	Lys
			20					25					30		
Asn	Gly	Phe	Gln	Gly	Pro	Leu	Pro	Gln	Arg	Gly	Leu				
			35					40							

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu	Val	Gln	Asp	Leu	Lys	Gly	Asp	Asp	Thr	Ala	Val	Arg	Thr	Ser	His
1				5					10					15	
Ser	Lys	Arg	Asp	Thr	Lys	Cys	Gln	Ser	Pro	Gly	Ser	Ser	Gly	Arg	Arg
			20					25					30		
Arg	Gly	Pro	Arg	Pro	His	Ser	Gly	Xaa	Ala	Cys	Cys	Gly	Pro	Gly	Ser
			35				40						45		

Gly Gly Gly Thr Trp Gly Val Ser Ser Trp His Cys Ser Val Ser Leu
 50 55 60
 Pro Lys Cys Ser His Ala Phe Ile Val Asp Phe Leu Tyr Phe Pro Phe
 65 70 75 80
 Ser Gly Glu Ala Ser Glu Arg Lys Arg Pro Asp Ser Gly Cys Ser Thr
 85 90 95
 Ser Lys Asp Thr Lys Tyr Gln Ser Val Tyr Val Ile Ser Glu Glu Lys
 100 105 110
 Asp Glu Cys Val Ile Ala
 115

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Thr Met Asn Asn Leu Ala Asn Cys Gln Arg Glu Lys Asp Ile Ser Val
 1 5 10 15
 Ser Ile Ile Gly Ala Thr Ser Asp Gln Glu His Gln Gln Glu Gly Gly
 20 25 30
 Leu Xaa Xaa Gly Gly Pro Xaa Pro Thr Arg Met Xaa Phe Lys Ala Arg
 35 40 45
 Tyr Pro Ser Val Asp Tyr Asn Ser Cys Arg Thr Ser Arg Val Thr Thr
 50 55 60
 Pro Pro Ser Gly Arg Arg Thr Ala Ser Val Thr Pro Ser Ala Ser Pro
 65 70 75 80
 Gln Ala Pro Gln Gly Gly Glu Gly Asp Pro Asp His Thr Gln Gly Xaa
 85 90 95
 Arg Ala Ala Gly Arg Ala Gln Glu Gly Val Pro Gly Gly Cys Leu Pro
 100 105 110
 Gly Thr Thr Ala Pro Phe Leu Phe Pro Asn Val Leu Met His Ser Leu
 115 120 125
 Trp Ile Phe Ser Ile Phe Leu Leu Val Glu Lys His Leu Lys Glu Lys
 130 135 140
 Gly Arg Thr Arg Ala Val Gln Leu Gln Lys Thr Pro Ser Thr Ser Arg
 145 150 155 160
 Cys Thr Ser Tyr Pro Arg Arg Arg Thr Ser Ala Ser Ser
 165 170

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Xaa Thr Trp Arg Thr Ala Ser Val Arg Arg Thr Ser Gln Ser Ala Ser
1 5 10 15
Ser Gly Xaa Arg Gln Ile Xaa Asn Thr Asn Lys Lys Ala Asp Phe Xaa
20 25 30
Xaa Gly Asp Xaa Ser Val Arg Gln Glu Trp Xaa Ser Arg Pro Ala Thr
35 40 45
Pro Ala Trp Thr Ile Thr Arg Ala Gly Pro Gln Gly
50 55 60

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Arg His Arg Arg Gln Asp Val Ala Gln Gln Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

His Gln Val Pro Val Pro Arg Leu Leu Arg Glu Glu Lys Gly Thr Pro
1 5 10 15
Thr Thr Leu Arg Gly Cys Val Leu Arg Ala Gly Leu Arg Arg Gly Tyr
20 25 30
Leu Gly Gly Val Phe Leu Glu Pro Leu Leu Arg Phe Ser Ser Gln Met
35 40 45
Phe Ser Cys Ile His Cys Gly Phe Ser Leu Phe Ser Phe
50 55 60

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Lys Lys Lys Ala Gly Leu Gly Leu Phe Asn Phe Lys Lys Arg His Gln
 1 5 10 15
 Val Pro Val Gly Val Arg His Ile Arg Gly Glu Gly Arg Val Arg His
 20 25 30
 Arg

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Thr Met Asn Asn Leu Ala Asn Cys Gln Arg Glu Lys Asp Ile Ser Val
 1 5 10 15
 Ser Ile Ile Gly Ala Thr Gly Ile Xaa Asn Thr Asn Lys Lys Ala Asp
 20 25 30
 Phe Xaa Xaa Gly Asp Xaa Ser Ser Asp Lys Asn Gly Phe Gln Lys Ala
 35 40 45
 Arg Tyr Pro Ser Val Asp Tyr Asn Leu Val Gln Asp Leu Lys Gly Asp
 50 55 60
 Asp Thr Ala Val Arg Thr Ser His Ser Lys Arg Asp Thr Lys Cys Gln
 65 70 75 80
 Ser Pro Gly Ser Ser Gly Arg Arg Arg Gly Pro Arg Pro His Ser Gly
 85 90 95
 Xaa Ala Cys Cys Gly Pro Gly Ser Gly Gly Gly Thr Trp Gly Val Ser
 100 105 110
 Ser Trp Asn His Cys Ser Val Ser Leu Pro Lys Cys Ser His Ala Phe
 115 120 125
 Ile Val Asp Phe Leu Tyr Phe Pro Phe Ser Gly Glu Ala Ser Glu Arg
 130 135 140
 Lys Arg Pro Asp Ser Gly Cys Ser Thr Ser Lys Asp Thr Lys Tyr Gln
 145 150 155 160
 Ser Val Tyr Val Ile Ser Glu Glu Lys Asp Glu Cys Val Ile Ala
 165 170 175

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2899 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTCCAGCGGT ACCATGGGCC GTCGGAGCGC GCTACCCCTT GCCGTGGTCT CTGCCCTGCT 60
 GTGCCAGGTC TGGAGCTCCG GCGTATTTGA GCTGAAGCTG CAGGAGTTCG TCAACAAGAA 120
 GGGGCTGCTG GGGAACCGCA ACTGCTGCCG CGGGGGCTCT GGCCCGCCTT GCGCCTGCAG 180
 GACCTTCTTT CGCGTATGCC TCAACCACTA CCAGGCCAGC GTGTCACCGG AGCCACCCTG 240

CACCTACGGC AGTGCTGTCA CGCCAGTGCT GGGTCTCGAC TCCTTCAGCC TGCCTSATKG 300
SGYASGSRYC SMCCYCGAGG YCKWCRGYAW CSMYAAGYYY GATATCGMMY TYCGGCTTCA 360
CCTGGCCRGG YACCTTCTCT CTGATYATTG AAGCYCTCCA YACAGAYTCT CCYGATGACC 420
TCGCAACAGA AAACCCAGAA AGACTCATCA GCCGCCTGRC CACYCAGAGG CACCTSACKG 480
TGGGMGARGA RTGGTCYCAG GACCTKCACA GYAGCGGCCG CACRGACCTC MRGTACTCYT 540
ACCGSTTYGT GTGTGACGAR CACTACTACG GAGARGGYTG CTCTGTKTTC TGCCGWCCYC 600
GGGAYGAYGC CTTYGGCCAC TTCACCTGYG GGGASMGWGG GGAGAARTG TGCRAACCCTG 660
GCTGGAAAGG SCMGTAAGTGC ACWGASCCRA TCTGYCTGCC WGGRTGTGAT GASCARCATG 720
GATWYTGTGA CAAACCAGGG GARTGCAAGT GCAGAGTKGG CTGGCAGGGC CGSTACTGYG 780
ATGAGTGYAT CCGYTAYCCA GGYTGTCTCC ATGGCACCTG CCAGCARCCC TGGCAGTGYA 840
ACTGCCAGGA AGGNTGGGGG GGCCTTTTCT GCAACCARGA CCTGAACTAC TGYACWCACC 900
ATAAGCCSTG CARGAATGGA GCCACCTGCA ACMAACACGG GCCAGGGGGA GCTACACWTG 960
KTCYTTGGCC GGNCYKGGGT AYANAGGGTG CCAMCTGYGA AGCTTGGGRA KTRGAYGAGT 1020
TGTTGMYCCY AGCCCYTGGY AAGAACGGAG SGAGCTKSAC GGAYCTTCGG AGRACAGCTW 1080
CTCYTGYACC TGCCCWCCCG GCTTCTAYGG CAARRTCTGT GARYTGAGYG CCATGACCTG 1140
TGCRGAYGGC CCTTGCTTYA AYGGRGWCG RTGYTCAGAY ARCCCYGAYG GAGGSTACAS 1200
CTGCCRYTGC CCKTGGGCT WCTCYGGCTT CAACTGTGAG AAGAARATKG AYYWCTGCRG 1260
CTCTTCMCCY TGTTCCTAAYG GTGCCAAGTG TGTGGACCTC GGYRAYKCYT ACCTGTGCCG 1320
STGCCAGGCY GGCTTCTCSG GGAGGYACTG YGASGACAA YGTGGAYGACT GYGCCTCCTC 1380
CCCGTGYGCM AAYGGGGGCA CCTGCCGGGA YRGYGTGAAC GACTTGTCTT GYACCTGCCC 1440
RCCTGGCTAC ACGGGCARGA ACTGCAGYGC CCCYGYCAGC AGGTGYGAGC AYGCACCCTG 1500
CCAYAATGGG GCCACCTGCC ACSAGAGGGG CCASCGCTAY WTGTGYGAGT GYGCCRRRG 1560
CTAYGSGGY CCCAACTGCC ANTTYCTGCT CCCYGAARCY GMCCMCCMG SCCCAYGGTG 1620
GTGGAAMCTC MSYKARARRM AYMTARRAGR GCCRGGSGG GCCCWTCCTC TKGGTGGYCG 1680
TGTGYGCCGG GGTSRTSCTT GTCCTCMTGC TGCTGCTGGG CTGTGCTGCT GTGGTGGTCT 1740
GCGTCCGGCT GARGCTRCAG AARCAACRG CYCCASCYGA MCCCTGNSGG GGRGAGACRG 1800
ARACCATGAA CAACCTRGNC AAYTGCCAGC GYGAGAAGGA CRTYTCWGTY AGCATCATYG 1860
GGGNYACSCA CATCAAGAAC ACCAACAAGA AGGCGGACTT YCACGGGGAC CAYRGNGCCR 1920
ASAAGARYRG CTTYAAGGYC CGMTACCCMR NKGTTGACTA TAACCTCGTK CRRGACCTCA 1980
AGGGWGAYGA MRCCRCSTC AGGGAYRCRC ACAGCAARCG TGACACCAAG TGNCAGYCMC 2040
AGRGCTCYKG AGGRGARGAG AAGGGGAYCS CCGACCMACA CTYAGGGGGT GGAGGAAGMW 2100
TCYTGAMAGA AAAAGGCCRG ASTYYGGGY TRYTCWACTT TCAAARGACA ANCMANGTAC 2160
MAGTCGGTGT NYGTYMTKTC YGNAGRAGGA AGGNTGASTG YGTYATAGGM RNYTGAGGTN 2220
GTAARNTGGN AGCGATGTGG CAANNTTCCC ATTTCTCKSA AAKNNNATTC CMMGGATATA 2280
GCYCCGNTGA ATGCTKCTGA GAGAGGAAGG GAGAGGAAAC CCAGGGACTG YTKYTCAGAA 2340
CCAGGTTTCA GCGAAGCTGG TTCTCTCAGA GTTAGCAGAG GCGCCCGACA CTGCCAGCCT 2400
AGGCTTTGGC TGCCGCTGGA CTGCCTGCTG GTTGTTCCTA TTGCACTATG GACAGTTGCT 2460
TTGAAGAGTA TATATTTAAA TGGACGAGTG ACTTGATTCA TATACGAAGC ACGCACTGCC 2520
CACACGTCTA TCTTGGATTA CTATGAGCCA GTCTTTCCTT GAACTAGAAA CACAACCTGCC 2580
TTTATTGTCC TTTTGTGATAC TGAGATGTGT TTTTTTTTTT CCTAGACGGG AAAAAGAAAA 2640
CGTGTGTTAT TTTTTTGGGA TTTGTAAAAA TATTTTTCAT GATATCTGTA AAGCTTGAGT 2700
ATTTTGTGAC GTTCATTTTT TTATAATTTA AATTTTGGTA AATATGTACA AAGGCACTTC 2760
GGGTCTATGT GACTATATTT TTTTGTATAT AAATGTATTT ATGGAATATT GTGCAAATGT 2820
TATTTGAGTT TTTTACTGTT TTGTTAATGA AGAAATTCAT TTTAAAATA TTTTCCAAA 2880
ATAAATATAA TGAACCTACA 2899

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Glu Lys Asp Glu Cys Val Ile Ala
1 5

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1981 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATTGGGTAC GGGCCCCCT CGAGGTCGAC GGTATCGATA AGCTTGATAT CGAATTCCGG 60
CTTCACCTGG CCGGGCACCT TCTCTCTGAT TATTGAAGCT CTCCACACAG ATTCTCCTGA 120
TGACCTCGCA ACAGAAAACC CAGAAAGACT CATCAGCCGC CTGGCCACCC AGAGGCACCT 180
GACGGTGGGC GAGGAGTGGT CCCAGGACCT GCACAGCAGC GGCCGCACGG ACCTCAAGTA 240
CTCCTACCGC TTCGTGTGTG ACGAACACTA CTACGGAGAG GGCTGCTCCG TTTTCTGCCG 300
TCCCCGGGAC GATGCCTTCG GCCACTTCAC CTGTGGGGAG CGTGGGGAGA AAGTGTGCAA 360
CCCTGGCTGG AAAGGGCCCT ACTGCACAGA GCCGATCTGC CTGCCTGGAT GTGATGAGCA 420
GCATGGATTT TGTGACAAAC CAGGGGAATG CAAGTGACAG GTGGGCTGGC AGGGCCGGTA 480
CTGTGACGAG TGTATCCGCT ATCCAGGCTG TCTCCATGGC ACCTGCCAGC AGCCCTGGCA 540
GTGCAACTGC CAGGAAGGNT GGGGGGGCCT TTTCTGCAAC CAGGACCTGA ACTACTGCAC 600
ACACCATAAG CCCTGCAAGA ATGGAGCCAC CTGCAACAAA CACGGGCCAG GGGGAGCTAC 660
ACTTGGTCTT TGGCCGNNCT GGGGTACANA GGGTGCCACC TCGGAAGCTT GGGGATTGGA 720
CGAGTTGTTG ACCCCAGCCC TTGGTAAGAA CGGAGGGAGC TTGACGGATC TTCGGAGAAC 780
AGCTACTCCT GTACCTGCCC ACCCGGCTTC TACGGCAAAA TCTGTGAATT GAGTGCCATG 840
ACCTGTGCGG ACGGCCCTTG CTTTAACGGG GGTGCGGTGCT CAGACAGCCC CGATGGAGGG 900
TACAGCTGCC GCTGCCCCGT GGGCTACTCC GGCTTCAACT GTGAGAAGAA AATTGACTAC 960
TGCAGCTCTT CACCCTGTTC TAATGGTGCC AAGTGTGTGG ACCTCGGTGA TGCCTACCTG 1020
TGCCGCTGCC AGGCCGGCTT CTCGGGGAGG CACTGTGACG ACAACGTGGA CGACTGCGCC 1080
TCCTCCCCGT GCGCCAACGG GGGCACCTGC CGGGATGGCG TGAACGACTT CTCCTGCACC 1140
TGCCCGCCTG GCTACACGGG CAGGAACTGC AGTGCCCCCG CCAGCAGGTG CGAGCACGCA 1200
CCCTGCCACA ATGGGGCCAC CTGCCACGAG AGGGGCCACC GCTATTTGTG CGAGTGTGCC 1260
CGAAGCTACG GGGGTCCCAA CTGCCANTTC CTGCTCCCCG AACTTGCCCC CCCGGCCCCA 1320
CGGTGGTGGA AACTCCCCTA AAAAAACCTA AAAGGGCCGG GGGGGGCCCA TCCCCTTGGT 1380
GGACGTGTGC GCCGGGGTCA TCCTTGTCCT CATGCTGCTG CTGGGCTGTG CCGCTGTGGT 1440
GGTCTGCGTC CGGCTGAGGC TGCAGAAGCA CCGGCCCCCA GCCGACCCCT GNCGGGGGGA 1500
GACGGAGACC ATGAACAACC TGGNCAACTG CCAGCGTGAG AAGGACATCT CAGTCAGCAT 1560
CATCGGGGNC ACGCAGATCA AGAACACCAA CAAGAAGGCG GACTTCCACG GGGACCACAG 1620
NGCCGACAAG AATGGCTTCA AGGCCCGCTA CCCAGNGGTG GACTATAACC TCGTGCAGGA 1680
CCTCAAGGGT GACGACACCG CCGTCAGGGA CGCGCACAGC AAGCGTGACA CCAAGTGNCA 1740
GCCCCAGGGC TCCTCAGGGG AGGAGAAGGG GACCCCCGAC CCACACTCAG GGGGTGGAGG 1800
AAGCATCTTG AAAGAAAAAG GCCGGACTTC GGGCTTGTTT AACTTTCAAA AGACAANCAA 1860
NGTACAAGTC GGTGTNCGTC ATTTCCGNAG GAGGAAGGNT GACTGCGTCA TAGGAANTTG 1920
AGGTNGTAAA NTGGNAGTTG ANNTTGGAAG GNNNTCCCCG GATTCCGNTT TCAAAGTTTT 1980
T 1981

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

His Trp Val Arg Ala Pro Leu Glu Val Asp Gly Ile Asp Lys Leu Asp
1 5 10 15
Ile Glu Phe Arg Leu His Leu Ala Gly His Leu Leu Ser Asp Tyr
20 25 30

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ser Ser Pro His Arg Phe Ser
1 5

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Pro Arg Asn Arg Lys Pro Arg Lys Thr His Gln Pro Pro Gly His Pro
1 5 10 15
Glu Ala Pro Asp Gly Gly Arg Gly Val Val Pro Gly Pro Ala Gln Gln
20 25 30
Arg Pro His Gly Pro Gln Val Leu Leu Pro Leu Arg Val
35 40 45

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Arg Thr Leu Leu Arg Arg Gly Leu Leu Arg Phe Pro Ser Pro Gly Arg
1 5 10 15

Cys Leu Arg Pro Leu His Leu Trp Gly Ala Trp Gly Glu Ser Val Gln
 20 25 30
 Pro Trp Leu Glu Arg Ala Leu Leu His Arg Ala Asp Leu Pro Ala Trp
 35 40 45
 Met

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Ala Ala Trp Ile Leu
 1 5

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Gln Thr Arg Gly Met Gln Val Gln Ser Gly Leu Ala Gly Pro Val Leu
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Arg Val Tyr Pro Leu Ser Arg Leu Ser Pro Trp His Leu Pro Ala Ala
 1 5 10 15
 Leu Ala Val Gln Leu Pro Gly Arg Xaa Gly Gly Pro Phe Leu Gln Pro
 20 25 30
 Gly Pro Glu Leu Leu His Thr Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ala Leu Gln Glu Trp Ser His Leu Gln Gln Thr Arg Ala Arg Gly Ser
1 5 10 15
Tyr Thr Trp Ser Leu Ala Gly Leu Gly Tyr Xaa Gly Cys His Leu Arg
20 25 30
Ser Leu Gly Ile Gly Arg Val Val Asp Pro Ser Pro Trp
35 40 45

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Glu Arg Arg Glu Leu Asp Gly Ser Ser Glu Asn Ser Tyr Ser Cys Thr
1 5 10 15
Cys Pro Pro Gly Phe Tyr Gly Lys Ile Cys Glu Leu Ser Ala Met Thr
20 25 30
Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Arg Cys Ser Asp Pro Asp
35 40 45
Gly Gly Tyr Ser Cys Arg Cys Pro Val Gly Tyr Ser Gly Phe Asn Cys
50 55 60
Glu Lys Lys Ile Asp Tyr Cys Ser Ser Ser Pro Cys Ser Asn Gly Ala
65 70 75 80
Lys Cys Val Asp Leu Gly Asp Ala Tyr Leu Cys Arg Gly Gln Ala Gly
85 90 95
Phe Ser Gly Arg His Cys Asp Asp Asn Val Asp Asp Cys Ala Ser Ser
100 105 110
Pro Cys Ala Asn Gly Gly Thr Cys Arg Asp Gly Val Asn Asp Phe Ser
115 120 125
Cys Thr Cys Pro Pro Gly Tyr Thr Gly Arg Asn Cys Ser Ala Pro Ala
130 135 140
Ser Arg Cys Glu His Ala Pro Cys His Asn Gly Ala Thr Cys His Glu
145 150 155 160
Arg Gly His Arg Tyr Xaa Cys Glu Cys Ala Arg Ser Tyr Gly Gly Pro
165 170 175
Asn Cys Xaa Phe Leu Leu Pro Glu Thr Ala Pro Pro Ala Pro Arg Trp
180 185 190
Trp Lys Leu Pro
195

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Lys Asn Leu Lys Gly Pro Gly Gly Ala His Pro Leu Gly Gly Arg Val
1 5 10 15
Arg Arg Gly His Pro Cys Pro His Ala Ala Ala Gly Leu Cys Arg Cys
20 25 30
Gly Gly Leu Arg Pro Ala Glu Ala Ala Glu Ala Pro Ala Pro Ser Arg
35 40 45
Pro Leu Xaa Gly Gly Asp Gly Asp His Glu Gln Pro Gly Gln Leu Pro
50 55 60
Ala
65

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Glu Gly His Leu Ser Gln His His Arg Gly His Ala Asp Gln Glu His
1 5 10 15
Gln Gln Glu Gly Gly Leu Pro Arg Gly Pro Gln Xaa Arg Gln Glu Trp
20 25 30
Leu Gln Gly Pro Leu Pro Xaa Gly Gly Leu
35 40

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Pro Arg Ala Gly Pro Gln Gly
1 5

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Arg His Arg Arg Gln Gly Arg Ala Gln Gln Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

His Gln Val Xaa Ala Pro Gly Leu Leu Arg Gly Gly Glu Gly Asp Pro
1 5 10 15
Arg Pro Thr Leu Arg Gly Trp Arg Lys His Leu Glu Arg Lys Arg Pro
20 25 30
Asp Phe Gly Leu Val Gln Leu Ser Lys Asp Xaa Gln Xaa Thr Ser Arg
35 40 45
Cys Xaa Ser Phe Pro Xaa Glu Glu Gly
50 55

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Leu Arg His Arg Xaa Leu Arg Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Xaa Trp Lys Xaa Xaa Pro Gly Phe Arg Phe Gln Ser Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ile Gly Tyr Gly Pro Pro Ser Arg Ser Thr Val Ser Ile Ser Leu Ile
1 5 10 15
Ser Asn Ser Gly Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu
20 25 30
Ala Leu His Thr Asp Ser Pro Asp Asp Leu Ala Thr Glu Asn Pro Glu
35 40 45
Arg Leu Ile Ser Arg Leu Ala Thr Gln Arg His Leu Thr Val Gly Glu
50 55 60
Glu Trp Ser Gln Asp Leu His Ser Ser Gly Arg Thr Asp Leu Lys Tyr
65 70 75 80
Ser Tyr Arg Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser
85 90 95
Val Phe Cys Arg Pro Arg Asp Asp Ala Phe Gly His Phe Thr Cys Gly
100 105 110
Glu Arg Gly Glu Lys Val Cys Asn Pro Gly Trp Lys Gly Pro Tyr Cys
115 120 125
Thr Glu Pro Ile Cys Leu Pro Gly Cys Asp Glu Gln His Gly Phe Cys
130 135 140
Asp Lys Pro Gly Glu Cys Lys Cys Arg Val Gly Trp Gln Gly Arg Tyr
145 150 155 160
Cys Asp Glu Cys Ile Arg Tyr Pro Gly Cys Leu His Gly Thr Cys Gln
165 170 175
Gln Pro Trp Gln Cys Asn Cys Gln Glu Gly Trp Gly Gly Leu Phe Cys
180 185 190
Asn Gln Asp Leu Asn Tyr Cys Thr His His Lys Pro Cys Lys Asn Gly
195 200 205
Ala Thr Cys Asn Lys His Gly Pro Gly Gly Ala Thr Leu Gly Leu Trp
210 215 220
Pro Xaa Trp Gly Thr Xaa Gly Ala Thr Cys Glu Ala Trp Gly Leu Asp
225 230 235 240
Glu Leu Leu Thr Pro Ala Leu Gly Lys Asn Gly Gly Ser Leu Thr Asp
245 250 255
Leu Arg Arg Thr Ala Thr Pro Val Pro Ala His Pro Ala Ser Thr Ala
260 265 270
Lys Ser Val Asn
275

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Pro Val Arg Thr Ala Leu Ala Leu Thr Gly Val Gly Ala Gln Thr Ala
1 5 10 15
Pro Met Glu Gly Thr Ala Ala Ala Ala Pro Trp Ala Thr Pro Ala Ser
20 25 30
Thr Val Arg Arg Lys Leu Thr Thr Ala Ala Leu His Pro Val Leu Met
35 40 45
Val Pro Ser Val Trp Thr Ser Val Met Pro Thr Cys Ala Ala Ala Arg
50 55 60
Pro Ala Ser Arg Gly Gly Thr Val Thr Thr Thr Trp Thr Thr Ala Pro
65 70 75 80
Pro Pro Arg Ala Pro Thr Gly Ala Pro Ala Gly Met Ala
85 90

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Thr Thr Ser Pro Ala Pro Ala Arg Leu Ala Thr Arg Ala Gly Thr Ala
1 5 10 15
Val Pro Pro Pro Ala Gly Ala Ser Thr His Pro Ala Thr Met Gly Pro
20 25 30
Pro Ala Thr Arg Gly Ala Thr Ala Ile Cys Ala Ser Val Pro Glu Ala
35 40 45
Thr Gly Val Pro Thr Ala Xaa Ser Cys Pro Lys Leu Pro Pro Arg Pro
50 55 60
His Gly Gly Gly Asn Ser Pro Lys Lys Thr
65 70

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Lys Gly Arg Gly Gly Pro Ile Pro Leu Val Asp Val Cys Ala Gly Val
1 5 10 15

Ile Leu Val Leu Met Leu Leu Leu Gly Cys Ala Ala Val Val Val Cys
 20 25 30
 Val Arg Leu Arg Leu Gln Lys His Arg Pro Pro Ala Asp Pro Xaa Arg
 35 40 45
 Gly Glu Thr Glu Thr Met Asn Asn Leu Xaa Asn Cys Gln Arg Glu Lys
 50 55 60
 Asp Ile Ser Val Ser Ile Ile Gly Xaa Thr Gln Ile Lys Asn Thr Asn
 65 70 75 80
 Lys Lys Ala Asp Phe His Gly Asp His Ala Asp Lys Asn Gly Phe Lys
 85 90 95
 Ala Arg Tyr Pro Xaa Val Asp Tyr Asn Leu Val Gln Asp Leu Lys Gly
 100 105 110
 Asp Asp Thr Ala Val Arg Asp Ala His Ser Lys Arg Asp Thr Lys Xaa
 115 120 125
 Gln Pro Gln Gly Ser Ser Gly Glu Glu Gly Thr Pro Asp Pro His Ser
 130 135 140
 Gly Gly Gly Gly Ser Ile Leu Lys Glu Lys Gly Arg Thr Ser Gly Leu
 145 150 155 160
 Phe Asn Phe Gln Lys Thr Xaa Xaa Val Gln Val Gly Val Arg His Phe
 165 170 175
 Arg Arg Arg Lys Xaa Asp Cys Val Ile Gly Xaa
 180 185

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Gly Xaa Lys Xaa Xaa Val Xaa Xaa Gly Lys Xaa Ser Pro Asp Ser Xaa
 1 5 10 15
 Phe Lys Val Phe
 20

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Leu Gly Thr Gly Pro Pro Arg Gly Arg Arg Tyr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Tyr Arg Ile Pro Ala Ser Pro Gly Arg Ala Pro Ser Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Leu Leu Lys Leu Ser Thr Gln Ile Leu Leu Met Thr Ser Gln Gln Lys
1 5 10 15
Thr Gln Lys Asp Ser Ser Ala Ala Trp Pro Pro Arg Gly Thr
20 25 30

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Arg Trp Ala Arg Ser Gly Pro Arg Thr Cys Thr Ala Ala Ala Arg
1 5 10 15
Thr Ser Ser Thr Pro Thr Ala Ser Cys Val Thr Asn Thr Thr Thr Glu
20 25 30
Arg Ala Ala Pro Phe Ser Ala Val Pro Gly Thr Met Pro Ser Ala Thr
35 40 45
Ser Pro Val Cys Ser Val Gly Arg Lys Cys Ala Thr Leu Ala Gly Lys
50 55 60
Gly Pro Thr Ala Gln Ser Arg Ser Ala Cys Leu Asp Val Met Ser Ser
65 70 75 80
Met Asp Phe Phe Val Thr Asn Gln Asn Ala Ser Ala Glu Trp Ala Gly
85 90 95
Arg Ala Gly Thr Val Thr Ser Val Ser Ala Ile Gln Ala Val Ser Met
100 105 110
Ala Pro Ala Ser Ser Pro Gly Ser Ala Thr Ala Arg Lys Xaa Gly Gly
115 120 125

Ala Phe Ser Ala Thr Arg Thr
130 135

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Thr Thr Ala His Thr Ile Ser Pro Ala Arg Met Glu Pro Pro Ala Thr
1 5 10 15
Asn Thr Gly Gln Gly Glu Leu His Leu Val Phe Gly Arg Xaa Gly Val
20 25 30
Xaa Arg Val Pro Pro Ala Lys Leu Gly Asp Trp Thr Ser Cys
35 40 45

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Pro Gln Pro Leu Val Arg Thr Glu Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Arg Ile Phe Gly Glu Gln Leu Leu Leu Tyr Leu Pro Thr Arg Leu Leu
1 5 10 15
Arg Gln Asn Leu
20

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ile Glu Cys His Asp Leu Cys Gly Arg Pro Leu Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Arg Gly Ser Val Leu Arg Gln Pro Arg Trp Arg Val Gln Leu Pro Leu
1 5 10 15
Pro Arg Gly Leu Leu Arg Leu Gln Leu
20 25

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Leu Leu Gln Leu Phe Thr Leu Phe
1 5

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Trp Cys Gln Val Cys Gly Pro Arg
1 5

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Cys Leu Pro Val Pro Leu Pro Gly Arg Leu Leu Gly Glu Ala Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Arg Gln Arg Gly Arg Leu Arg Leu Leu Pro Val Arg Gln Gly His Leu
1 5 10 15
Pro Gly Trp Arg Glu Arg Leu Leu Leu His Leu Pro Ala Trp Leu His
20 25 30
Gly Gln Glu Leu Gln Cys Pro Arg Gln Gln Val Arg Ala Arg Thr Leu
35 40 45
Pro Gln Trp Gly His Leu Pro Arg Glu Gly Pro Pro Leu Phe Val Arg
50 55 60
Val Cys Pro Lys Leu Arg Gly Ser Gln Leu Pro Xaa Pro Ala Pro Arg
65 70 75 80
Asn Cys Pro Pro Gly Pro Thr Val Val Glu Thr Pro Leu Lys Lys Pro
85 90 95
Lys Arg Ala Gly Gly Gly Pro Ser Pro Trp Trp Thr Cys Ala Pro Gly
100 105 110
Ser Ser Leu Ser Ser Cys Cys Cys Trp Ala Val Pro Leu Trp Trp Ser
115 120 125
Ala Ser Gly
130

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Gly Cys Arg Ser Thr Gly Pro Gln Pro Thr Pro Xaa Gly Gly Arg Arg
 1 5 10 15
 Arg Pro

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Thr Thr Trp Xaa Thr Ala Ser Val Arg Arg Thr Ser Gln Ser Ala Ser
 1 5 10 15
 Ser Gly Xaa Arg Arg Ser Arg Thr Pro Thr Arg Arg Arg Thr Ser Thr
 20 25 30
 Gly Thr Thr Xaa Pro Thr Arg Met Ala Ser Arg Pro Ala Thr Gln Xaa
 35 40 45
 Trp Thr Ile Thr Ser Cys Arg Thr Ser Arg Val Thr Thr Pro Pro Ser
 50 55 60
 Gly Thr Arg Thr Ala Ser Val Thr Pro Ser Xaa Ser Pro Arg Ala Pro
 65 70 75 80
 Gln Gly Arg Arg Arg Cys Pro Pro Thr His Thr Gln Gly Val Glu Glu
 85 90 95
 Ala Ser

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Lys Lys Lys Ala Gly Leu Arg Ala Cys Ser Thr Phe Lys Arg Gln Xaa
 1 5 10 15
 Xaa Tyr Lys Ser Val Xaa Val Ile Ser Xaa Gly Gly Arg Xaa Thr Ala
 20 25 30
 Ser

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Glu Xaa Glu Val Val Xaa Trp Xaa Leu Xaa Leu Glu Xaa Xaa Pro Arg
1 5 10 15
Ile Pro Xaa Ser Lys Phe
20

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Gly Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Ala Leu His
1 5 10 15
Thr Asp Ser Pro Asp Asp Leu Ala Thr Glu Asn Pro Glu Arg Leu Ile
20 25 30
Ser Arg Leu Ala Thr Gln Arg His Leu Thr Val Gly Glu Glu Trp Ser
35 40 45
Gln Asp Leu His Ser Ser Gly Arg Thr Asp Leu Lys Tyr Ser Tyr Arg
50 55 60
Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys
65 70 75 80
Arg Pro Arg Asp Asp Ala Phe Gly His Phe Thr Cys Gly Glu Arg Gly
85 90 95
Glu Lys Val Cys Asn Pro Gly Trp Lys Gly Pro Tyr Cys Thr Glu Pro
100 105 110
Ile Cys Leu Pro Gly Cys Asp Glu Gln His Gly Phe Cys Asp Lys Pro
115 120 125
Gly Glu Cys Lys Cys Arg Val Gly Trp Gln Gly Arg Tyr Cys Asp Glu
130 135 140
Cys Ile Arg Tyr Pro Gly Cys Leu His Gly Thr Cys Gln Gln Pro Trp
145 150 155 160
Gln Cys Asn Cys Gln Glu Gly Trp Gly Gly Leu Phe Cys Asn Gln Asp
165 170 175
Leu Asn Tyr Cys Thr His His Lys Pro Cys Lys Asn Gly Ala Thr Cys
180 185 190

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Thr Asn Thr Gly Gln Gly
1 5

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Lys Asn Gly Gly Ser Leu Thr Asp Leu
1 5

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Glu Asn Ser Tyr Ser Cys Thr Cys Pro Pro Gly Phe Tyr Gly Lys Ile
1 5 10 15
Cys Glu Leu Ser Ala Met Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly
20 25 30
Gly Arg Cys Ser Asp Ser Pro Asp Gly Gly Tyr Ser Cys Arg Cys Pro
35 40 45
Val Gly Tyr Ser Gly Phe Asn Cys Glu Lys Lys Ile Asp Tyr Cys Ser
50 55 60
Ser Ser Pro Cys Ser Asn Gly Ala Lys Cys Val Asp Leu Gly Asp Ala
65 70 75 80
Tyr Leu Cys Arg Cys Gln Ala Gly Phe Ser Gly Arg His Cys Asp Asp
85 90 95
Asn Val Asp Asp Cys Ala Ser Ser Pro Cys Ala Asn Gly Gly Thr Cys
100 105 110
Arg Asp Gly Val Asn Asp Phe Ser Cys Thr Cys Pro Pro Gly Tyr Thr
115 120 125
Gly Arg Asn Cys Ser Ala Pro Ala Ser Arg Cys Glu His Ala Pro Cys
130 135 140
His Asn Gly Ala Thr Cys His Glu Arg Gly His Arg Tyr
145 150 155

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Cys Glu Cys Ala Arg Ser Tyr Gly Gly Pro Asn Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Phe Leu Leu Pro Glu
1 5

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Pro Pro Gly Pro
1

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Leu Leu Leu Gly Cys Ala Ala Val Val Val Cys Val Arg Leu Arg Leu
1 5 10 15
Gln Lys His Arg Pro Pro Ala Asp Pro
20 25

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Arg Gly Glu Thr Glu Thr Met Asn Asn Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Asn Cys Gln Arg Glu Lys Asp Ile Ser Val Ser Ile Ile Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Thr Gln Ile Lys Asn Thr Asn Lys Lys Ala Asp Phe His Gly Asp His
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ala Asp Lys Asn Gly Phe Lys Ala Arg Tyr Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Val Asp Tyr Asn Leu Val Gln Asp Leu Lys Gly Asp Asp Thr Ala Val
1 5 10 15
Arg Asp Ala His Ser Lys Arg Asp Thr Lys
20 25

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Gln Pro Gln Gly Ser Ser Gly Glu Glu Lys Gly Thr Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Pro Thr Leu Arg
1

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Arg Lys Arg Pro

1

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 6
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 12
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 18
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 21
- (D) OTHER INFORMATION: N=Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTCGGNTTYA CNTGGCCNGG NAC

23

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 3
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 9
- (D) OTHER INFORMATION: N=Inosine

(A) NAME/KEY: Modified Base
(B) LOCATION: 12
(D) OTHER INFORMATION: N=Inosine

(A) NAME/KEY: Modified Base
(B) LOCATION: 15
(D) OTHER INFORMATION: N=Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

TCNATGCANG TNCCNCCRTT

20

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Phe Gly Phe Thr Trp Pro Gly Thr
1 5

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Asn Gly Gly Thr Cys Ile Asp
1 5

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Ser Ile Pro Pro Gly Ser Arg Thr Ser Leu Gly Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 3
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 9
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 15
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 18
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 21
- (D) OTHER INFORMATION: N=Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GGNTTCACNT GGCCNGGNAC NTT

23

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 3
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 6
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 18
- (D) OTHER INFORMATION: N=Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTNCCNCCRT TYTTRCANGG RTT

23

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Asn Pro Cys Lys Asn Gly Gly Thr
1 5

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 3
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 15
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 18
- (D) OTHER INFORMATION: N=Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ACNATGAAYA AYCTNGCNAA YTG

23

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Thr Met Asn Asn Leu Ala Asn Cys
1 5

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 6
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 9
- (D) OTHER INFORMATION: N=Inosine

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 21
- (D) OTHER INFORMATION: N=Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

ACRTANACNG AYTGR TAYTT NGT

23

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Thr Lys Tyr Gln Ser Val Tyr Val
1 5

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA
(ix) FEATURE:

- (A) NAME/KEY: Modified Base
(B) LOCATION: 6
(D) OTHER INFORMATION: N=Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GCDATNACRC AYTCTCYTT YTC

23

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Gly Phe Thr Trp Pro Gly Thr Phe
1 5